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OM protein - protein search, using sw model

Run on: December 9, 2003, 14:05:49 ; Search time 21 Seconds  
(without alignments)  
40.296 Million cell updates/sec

Title: US-09-651-685A-5

Perfect score: 114  
Sequence: 1 CCYDASVNDTCGEORAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgm2\_6/ptodata/1/1aa/5A.COMB.pep:\*\n2: /cgm2\_6/ptodata/1/1aa/5B.COMB.pep:\*\n3: /cgm2\_6/ptodata/1/1aa/6A.COMB.pep:\*\n4: /cgm2\_6/ptodata/1/1aa/6B.COMB.pep:\*\n5: /cgm2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*\n6: /cgm2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	109	95.6	73	4	US-09-037-094-3	Sequence 3, Appl1
2	109	95.6	74	1	US-08-463-224-3	Sequence 3, Appl1
3	109	95.6	74	2	US-08-463-377-3	Sequence 3, Appl1
4	109	95.6	74	3	US-09-246-5008-10	Sequence 10, Appl1
5	109	95.6	1676	4	US-08-467-283A-2	Sequence 2, Appl1
6	94	82.5	74	3	US-09-246-5008-12	Sequence 11, Appl1
7	93	81.6	74	3	US-09-246-5008-11	Sequence 11, Appl1
8	88	77.2	77	3	US-09-246-5008-14	Sequence 14, Appl1
9	84	73.7	77	3	US-09-246-5008-13	Sequence 13, Appl1
10	55.5	48.7	76	3	US-09-246-5008-8	Sequence 8, Appl1
11	51.5	45.2	77	3	US-09-246-5008-6	Sequence 6, Appl1
12	50.5	44.3	77	3	US-09-246-5008-7	Sequence 7, Appl1
13	48.5	42.5	76	3	US-09-246-5008-9	Sequence 9, Appl1
14	44	38.6	237	4	US-09-328-352-8181	Sequence 8181, Appl1
15	43.5	38.2	1651	1	US-08-447-411-2	Sequence 2, Appl1
16	42	36.8	71	2	US-08-972-008-4	Sequence 4, Appl1
17	42	36.8	71	4	US-09-267-409-4	Sequence 4, Appl1
18	42	36.8	241	3	US-08-808-148-1	Sequence 11, Appl1
19	42	36.8	241	3	US-09-020-956-114	Sequence 114, Appl1
20	42	36.8	241	3	US-09-030-907-114	Sequence 114, Appl1
21	42	36.8	241	4	US-09-439-313-114	Sequence 114, Appl1
22	42	36.8	241	4	US-09-352-616A-114	Sequence 114, Appl1
23	42	36.8	241	4	US-09-232-149A-114	Sequence 114, Appl1
24	42	36.8	263	2	US-08-972-008-2	Sequence 2, Appl1
25	42	36.8	263	4	US-09-141-027-2	Sequence 2, Appl1
26	42	36.8	263	4	US-09-267-409-2	Sequence 2, Appl1
27	42	36.8	263	4	US-09-617-804-2	Sequence 2, Appl1

28	41.5	36.4	486	4	US-09-914-259-35	Sequence 35, Appl
29	41.5	36.4	1333	1	US-08-447-411-76	Sequence 76, Appl
30	41.5	36.4	1333	2	US-08-662-227-34	Sequence 34, Appl
31	41.5	36.4	1333	4	US-09-017-947-34	Sequence 34, Appl
32	41	36.0	363	2	US-08-483-101-16	Sequence 16, Appl
33	41	36.0	641	4	US-09-687-538B-8	Sequence 8, Appl
34	40	35.1	115	4	US-09-107-532A-6191	Sequence 6191, Ap
35	40	35.1	160	4	US-09-252-991A-22711	Sequence 22711, A
36	40	35.1	289	4	US-09-107-532A-4580	Sequence 4580, Ap
37	40	35.1	751	2	US-08-836-443-3	Sequence 3, Appl
38	40	35.1	802	4	US-09-632-098-2	Sequence 2, Appl
39	40	35.1	812	4	US-09-632-098-4	Sequence 4, Appl
40	40	35.1	1940	2	US-08-644-271-30	Sequence 30, Appl
41	40	35.1	1940	4	US-09-077-955-34	Sequence 34, Appl
42	40	35.1	4544	1	US-08-469-486-52	Sequence 52, Appl
43	40	35.1	4544	2	US-08-469-658-52	Sequence 52, Appl
44	39.5	34.6	256	4	US-09-325-932A-57	Sequence 57, Appl
45	39	34.2	34	2	US-08-867-087B-64	Sequence 64, Appl

## ALIGNMENTS

```
RESULT 1
US-09-097-094-3
; Sequence 3, Application US/09097094
; Patent No. 6326468
; GENERAL INFORMATION:
; APPLICANT: Canne, Lynne
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Simon, Reyna
; TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
; TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
; TITLE OF INVENTION: Solution
; FILE REFERENCE: GREN-023/01US
; CURRENT APPLICATION NUMBER: US/09/097,094
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: 60/049,553
; EARLIER FILING DATE: 1997-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-094-3

Query Match          95.6% Score 109; DB 4; Length 73;
Best Local Similarity 95.0% Pred. No. 8e-10; 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCYDASVNDTCGEORAR 20
DB      20 CCYDASVNDTCGEORAR 39

RESULT 2
US-08-463-224-3
; Sequence 3, Application US/08463224
; Patent No. 5807824
; GENERAL INFORMATION:
; APPLICANT: van Oostrum, Jan
; APPLICANT: Boyar, William C.
; APPLICANT: Galakatos, Nicholas G.
; APPLICANT: Schmitz, Albert
; APPLICANT: van Heeke, Gino
; TITLE OF INVENTION: C5a Receptor Antagonists Having
; TITLE OF INVENTION: Substantially No. 5807824Agonist Activity
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lemner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
```

```
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-224-3

Query Match          95.6%; Score 109; DB 1; Length 74;
Best Local Similarity 95.0%; Pred. No. 8.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEQRAAR 20
Db      21 CCYDGACVNNDETCEQRAAR 40

RESULT 3
US-08-463-377-3
Sequence 3, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oosterum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499A agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-377-3

Query Match          95.6%; Score 109; DB 2; Length 74;
Best Local Similarity 95.0%; Pred. No. 8.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEQRAAR 20
Db      21 CCYDGACVNNDETCEQRAAR 40

RESULT 4
US-09-246-500B-10
Sequence 10, Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugli, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
TITLE OF INVENTION: Using the Substrates
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 74
TYPE: PRT
ORGANISM: Human C5a Anaphylatoxin
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (64)...(66)
US-09-246-500B-10

Query Match          95.6%; Score 109; DB 3; Length 74;
Best Local Similarity 95.0%; Pred. No. 8.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEQRAAR 20
Db      21 CCYDGACVNNDETCEQRAAR 40

RESULT 5
US-08-487-283A-2
Sequence 2, Application US/08487283A
Patent No. 6355245
GENERAL INFORMATION:
APPLICANT: Evans, Mark J.
APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park (Alexion)
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4mb storage
```

```
COMPUTER: Macintosh Celris 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)776-1790
TELEFAX: (203)772-3655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1676 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Pro-CS Polypeptide
HYPOTHEetical: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Haviland, D.L.
AUTHORS: Haviland, J.C.
AUTHORS: Fleischer, D.T.
AUTHORS: Hunt, A.
AUTHORS: Wetzel, R.A.
TITLE: Complete cDNA Sequence of Human
Patent No. 6355245
JOURNAL: Journal of Immunology
VOLUME: 146
PAGES: 362-368
DATE: 1991
US-08-487-283A-2

Query Match          95.6%; Score 109; DB 4; Length 1676;
Best Local Similarity 95.0%; Pred. No. 2.3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CCYDASVNDTCERQRAAR 20
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Db 698 CCYDAGVNDTCERQRAAR 717
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RESULT 6
US-09-246-500B-12
; Sequence 12, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Cow C5a Anaphylatoxin
US-09-246-500B-12
Query Match          82.5%; Score 94; DB 3; Length 74;
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Best Local Similarity 80.0%; Pred. No. 1.6e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CCYDASVNDTCERQRAAR 20
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Db 21 CCYDGAHRNDETCERQRAAR 40
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```
RESULT 7
US-09-246-500B-11
; Sequence 11, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Pig C5a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (64)...(66)
US-09-246-500B-11
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Query Match          81.6%; Score 93; DB 3; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CCYDASVNDTCERQRAAR 20
    |||||:|||||:|||||
Db 21 CCYDGAHRNDETCERQRAAR 40
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```
RESULT 8
US-09-246-500B-14
; Sequence 14, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse C5a Anaphylatoxin
US-09-246-500B-14
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Query Match          77.2%; Score 88; DB 3; Length 77;
Best Local Similarity 80.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CCYDASVNDTCERQRAAR 20
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Db 24 CCYDGAHRNDETCERQRAAR 43
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RESULT 9
US-09-246-500B-13
; Sequence 13, Application US/09246500B
; Patent No. 6235494
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/ GENERAL INFORMATION:
/ APPLICANT: Hugli, Tony E.
/ TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
/ TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
/ TITLE OF INVENTION: Using the Substrates
/ FILE REFERENCE: 24730-2204
/ CURRENT APPLICATION NUMBER: US/09/246,500B
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Rat C5a Anaphylatoxin
/ FEATURE:
/ NAME/KEY: CARBOHYD
/ LOCATION: (67)...(69)
US-09-246-500B-13

Query Match          73.7% Score 84; DB 3; Length 77;
Best Local Similarity 75.0%; Pred. No. 5.6e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEORAA 20
Db      24 CCYDARENKYETCEORVAR 43

RESULT 10
US-09-246-500B-8
/ Sequence 8, Application US/09246500B
/ Patent No. 6235494
/ GENERAL INFORMATION:
/ APPLICANT: Hugli, Tony E.
/ TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
/ TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
/ FILE REFERENCE: 24730-2204
/ CURRENT APPLICATION NUMBER: US/09/246,500B
/ CURRENT FILING DATE: 1999-02-08
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 76
/ TYPE: PRT
/ ORGANISM: Rat C4a Anaphylatoxin
/ FEATURE:
/ NAME/KEY: CARBOHYD
/ LOCATION: (66)...(68)
US-09-246-500B-8

Query Match          48.7% Score 55.5; DB 3; Length 76;
Best Local Similarity 57.1%; Pred. No. 0.13;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY      1 CCYDGASVNNDETCEORAA 20
Db      23 CCODGKTLPMARTEORAA 43

RESULT 11
US-09-246-500B-6
/ Sequence 6, Application US/09246500B
/ Patent No. 6235494
/ GENERAL INFORMATION:
/ APPLICANT: Hugli, Tony E.
/ TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
/ TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
/ FILE REFERENCE: 24730-2204
/ CURRENT APPLICATION NUMBER: US/09/246,500B
/ CURRENT FILING DATE: 1999-02-08
/ NUMBER OF SEQ ID NOS: 19
```

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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Human C4a Anaphylatoxin
/ US-09-246-500B-6

Query Match          45.2% Score 51.5; DB 3; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.53;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      1 CCYDGAS-VNNDETCEORAA 20
Db      23 CCODGVTPLPMRSCORAA 43

RESULT 12
US-09-246-500B-7
/ Sequence 7, Application US/09246500B
/ Patent No. 6235494
/ GENERAL INFORMATION:
/ APPLICANT: Hugli, Tony E.
/ TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
/ TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
/ FILE REFERENCE: 24730-2204
/ CURRENT APPLICATION NUMBER: US/09/246,500B
/ CURRENT FILING DATE: 1999-02-08
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Cow C4a Anaphylatoxin
/ US-09-246-500B-7

Query Match          44.3% Score 50.5; DB 3; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.75;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      1 CCYDGAS-VNNDETCEORAA 20
Db      23 CCODGVTPLPMRSCORAA 43

RESULT 13
US-09-246-500B-9
/ Sequence 9, Application US/09246500B
/ Patent No. 6235494
/ GENERAL INFORMATION:
/ APPLICANT: Hugli, Tony E.
/ TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
/ TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
/ FILE REFERENCE: 24730-2204
/ CURRENT APPLICATION NUMBER: US/09/246,500B
/ CURRENT FILING DATE: 1999-02-08
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 76
/ TYPE: PRT
/ ORGANISM: Mouse C4a Anaphylatoxin
/ FEATURE:
/ NAME/KEY: CARBOHYD
/ LOCATION: (66)...(68)
US-09-246-500B-9

Query Match          42.5% Score 48.5; DB 3; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      1 CCYDGAS-VNNDETCEORAA 19
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Db 23 CCODGVTRLPMKRCSCORAA 42

RESULT 14  
US-09-328-352-8181  
; Sequence 8181, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 8181  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-8181

Query Match 38.6%; Score 44; DB 4; Length 237;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVNDERCE 15  
Db 221 DDAVACNDERCD 232

RESULT 15  
US-08-447-411-2  
; Sequence 2, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRITZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/043,747  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5773243man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-101-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1651 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-447-411-2

Query Match 38.2%; Score 43.5; DB 1; Length 1651;  
Best Local Similarity 52.6%; Pred. No. 2.3e+02;  
Matches 10; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDGASVN-NDETCEORA 18  
Db 683 CCEDGKHENPMGTYTCKRA 701

Search completed: December 9, 2003, 14:08:59  
Job time: 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 14:07:54 ; Search time 30 Seconds

(without alignments)  
123.989 Million cell updates/sec

Title: US-09-651-685A-5

Perfect score: 114  
Sequence: 1 CCYDASVNDTCCEQRAAR 20

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	10	US-09-878-603-5 Sequence 5, Appli
2	114	100.0	74	10	US-09-878-603-3 Sequence 3, Appli
3	111	97.4	20	10	US-09-878-603-68 Sequence 68, Appli
4	110	96.5	20	10	US-09-878-603-67 Sequence 67, Appli
5	110	96.5	20	10	US-09-878-603-69 Sequence 69, Appli
6	110	96.5	20	10	US-09-878-603-70 Sequence 70, Appli
7	110	96.5	20	10	US-09-878-603-71 Sequence 71, Appli
8	110	96.5	20	10	US-09-878-603-73 Sequence 73, Appli
9	109	95.6	19	10	US-09-878-603-54 Sequence 54, Appli
10	109	95.6	73	10	US-09-987-655-3 Sequence 3, Appli
11	109	95.6	73	10	US-09-987-675-3 Sequence 3, Appli
12	109	95.6	1251	9	US-09-778-927A-58 Sequence 58, Appli
13	109	95.6	1602	9	US-09-778-927A-59 Sequence 59, Appli
14	108	94.7	20	10	US-09-878-603-64 Sequence 64, Appli
15	108	94.7	20	10	US-09-878-603-65 Sequence 65, Appli

16	106	93.0	20	10	US-09-878-603-72 Sequence 72, Appli
17	105	92.1	18	10	US-09-878-603-55 Sequence 55, Appli
18	105	92.1	19	10	US-09-878-603-59 Sequence 59, Appli
19	102	89.5	20	10	US-09-878-603-66 Sequence 66, Appli
20	101	88.6	17	10	US-09-878-603-56 Sequence 56, Appli
21	98	86.0	20	10	US-09-878-603-74 Sequence 74, Appli
22	96	84.2	16	10	US-09-878-603-57 Sequence 57, Appli
23	96	84.2	18	10	US-09-878-603-60 Sequence 60, Appli
24	94	82.5	74	10	US-09-878-603-7 Sequence 7, Appli
25	93	81.6	74	10	US-09-878-603-8 Sequence 8, Appli
26	91	79.8	15	10	US-09-878-603-58 Sequence 58, Appli
27	89	78.1	17	10	US-09-878-603-61 Sequence 61, Appli
28	85	74.6	354	14	US-10-039-050-2 Sequence 2, Appli
29	84	73.7	77	10	US-09-878-603-1 Sequence 1, Appli
30	83	72.8	16	10	US-09-878-603-62 Sequence 62, Appli
31	77	67.5	15	10	US-09-878-603-63 Sequence 63, Appli
32	51	44.7	20	10	US-09-878-603-2 Sequence 2, Appli
33	45	39.5	141	12	US-10-238-075-831 Sequence 831, App
34	44	38.6	715	12	US-10-021-660-110 Sequence 110, App
35	44	38.6	884	12	US-10-032-585-7212 Sequence 7212, Ap
36	43.5	38.2	241	15	US-10-097-340-326 Sequence 326, App
37	43.5	38.2	241	15	US-10-205-823-425 Sequence 425, App
38	42	36.8	233	10	US-09-981-878-137 Sequence 137, App
39	42	36.8	233	11	US-09-148-545-137 Sequence 137, App
40	42	36.8	241	9	US-09-759-143-114 Sequence 114, App
41	42	36.8	241	9	US-09-780-669-114 Sequence 114, App
42	42	36.8	241	9	US-09-030-606-114 Sequence 114, App
43	42	36.8	241	9	US-09-822-827-114 Sequence 114, App
44	42	36.8	241	9	US-09-115-453-114 Sequence 114, App
45	42	36.8	241	10	US-09-232-880-114 Sequence 114, App

#### ALIGNMENTS

RESULT 1  
US-09-878-603-5  
; Sequence 5, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarmak, Vidya  
; APPLICANT: Czermak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: US-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-878-603-5

Query Match 100.0%; Score 114; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDASVNDTCCEQRAAR 20  
DB 1 CCYDASVNDTCCEQRAAR 20

RESULT 2  
US-09-878-603-3  
; Sequence 3, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.

```
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-878-603-3

Query Match          100.0%; Score 114; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEORAR 20
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Db      21 CCYDGASVNNDETCEORAR 40

RESULT 3
US-09-878-603-68
; Sequence 68, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-878-603-68

Query Match          97.4%; Score 111; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEORAR 20
        |||||
Db      1 CCYDGATVNNDETCEORAR 20

RESULT 4
US-09-878-603-67
; Sequence 67, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
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; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-878-603-67

Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEORAR 20
        |||||
Db      1 CCYDGASVNNDETCEORAR 20

RESULT 5
US-09-878-603-69
; Sequence 69, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-878-603-69

Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCYDGASVNNDETCEORAR 20
        |||||
Db      1 CCYDGASVNNDETCEORAR 20

RESULT 6
US-09-878-603-70
; Sequence 70, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
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LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-70

Query Match  
Best Local Similarity 96.5%; Score 110; DB 10; Length 20;  
Pred. No. 4.2e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 7  
US-09-878-603-71  
Sequence 71, Application US/09878603  
Patent No. US20020165138A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Peter A.  
APPLICANT: Huber-Lang, Markus  
APPLICANT: Sarma, Vidya  
APPLICANT: Czermak, Boris  
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
FILE REFERENCE: UM-03783  
CURRENT APPLICATION NUMBER: US/09/878,603  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 09/387,671  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 71  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-71

Query Match  
Best Local Similarity 96.5%; Score 110; DB 10; Length 20;  
Pred. No. 4.2e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 8  
US-09-878-603-73  
Sequence 73, Application US/09878603  
Patent No. US20020165138A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Peter A.  
APPLICANT: Huber-Lang, Markus  
APPLICANT: Sarma, Vidya  
APPLICANT: Czermak, Boris  
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
FILE REFERENCE: UM-03783  
CURRENT APPLICATION NUMBER: US/09/878,603  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 09/387,671  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 73  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-878-603-73

Query Match  
Best Local Similarity 96.5%; Score 110; DB 10; Length 20;  
Pred. No. 4.2e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 9  
US-09-878-603-54  
Sequence 54, Application US/09878603  
Patent No. US20020165138A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Peter A.  
APPLICANT: Huber-Lang, Markus  
APPLICANT: Sarma, Vidya  
APPLICANT: Czermak, Boris  
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
FILE REFERENCE: UM-03783  
CURRENT APPLICATION NUMBER: US/09/878,603  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 09/387,671  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 54  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-54

Query Match  
Best Local Similarity 96.6%; Score 109; DB 10; Length 19;  
Pred. No. 5.6e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAA 19  
Db 1 CCYDASVNNDETCEQRAA 19

RESULT 10  
US-09-987-655-3  
Sequence 3, Application US/09987655  
Patent No. US20020132975A1  
GENERAL INFORMATION:  
APPLICANT: Canne, Lynne  
APPLICANT: Kent, Stephen B.H.  
APPLICANT: Simon, Reyna  
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or  
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous  
FILE REFERENCE: GREN-023/01US  
CURRENT APPLICATION NUMBER: US/09/987,655  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 09/097,094  
PRIOR FILING DATE: 1998-06-12  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-987-655-3

Query Match  
Best Local Similarity 95.6%; Score 109; DB 10; Length 73;  
Pred. No. 2.4e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 CCYDGASVNNDETCEORAR 20  
Db 20 CCYDGACVNNDETCEORAR 39

## RESULT 11

US-09-987-675-3  
; Sequence 3, Application US/09987675  
; Patent No. US20020169282A1  
; GENERAL INFORMATION:  
; APPLICANT: Canne, Lynne  
; APPLICANT: Kent, Stephen B.H.  
; APPLICANT: Simon, Reyna  
; TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or  
; TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous  
; TITLE OF INVENTION: Solution  
; FILE REFERENCE: GRFN-023/01US  
; CURRENT APPLICATION NUMBER: US/09/987,675  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 09/097,094  
; PRIOR FILING DATE: 1998-06-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-987-675-3

Query Match 95.6%; Score 109; DB 10; Length 73;  
Best Local Similarity 95.0%; Pred. No. 2,4e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
Db 20 CCYDGACVNNDETCEORAR 39

## RESULT 12

US-09-778-927A-58  
; Sequence 58, Application US/09778927A  
; Patent No. US20020068342A1  
; GENERAL INFORMATION:  
; APPLICANT: KHOSRAVI, Ramj et al.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCE: 2786-0160P  
; CURRENT APPLICATION NUMBER: US/09/778,927A  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: IL 134453  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: IL13541  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 1251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1251)  
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other  
US-09-778-927A-58

Query Match 95.6%; Score 109; DB 9; Length 1251;  
Best Local Similarity 95.0%; Pred. No. 5e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
Db 698 CCYDGACVNNDETCEORAR 717

RESULT 13  
US-09-778-927A-59  
; Sequence 59, Application US/09778927A  
; Patent No. US20020068342A1  
; GENERAL INFORMATION:  
; APPLICANT: KHOSRAVI, Ramj et al.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCE: 2786-0160P  
; CURRENT APPLICATION NUMBER: US/09/778,927A  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: IL 134453  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: IL13541  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 1602  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1602)  
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other  
US-09-778-927A-59

Query Match 95.6%; Score 109; DB 9; Length 1602;  
Best Local Similarity 95.0%; Pred. No. 6,5e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
Db 698 CCYDGACVNNDETCEORAR 717

RESULT 14  
US-09-878-603-64  
; Sequence 64, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Salma, Vidya  
; APPLICANT: Czernak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-64

Query Match 94.7%; Score 108; DB 10; Length 20;  
Best Local Similarity 95.0%; Pred. No. 8,4e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
Db 1 CCYDGASVNNDETCEORAR 20

RESULT 15  
US-09-878-603-65

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Sequence 65, Application US/09978603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/381,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ. ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 20
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65

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Query Match	94.7%;	Score 108;	DB 10;	length 20;
Best Local Similarity	95.0%;	Pred. No. 8.4e-10;		
Matches	19;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY	1	CCYDGASVNNDETCEQRAAR	20
Dp	1	CCYDGASVNNQETCEQRAAR	20

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Search completed: December 9, 2003, 14:13:18
Job time : 30 secs
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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 9, 2003, 14:05:42 ; Search time 41 Seconds

(without alignments)  
77.428 Million cell updates/sec

Title: US-09-651-685A-5

Perfect score: 114  
Sequence: 1 CCYDASVNDCTCQRAAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	114	100.0	20	22	AA074055 Human C5a peptide
2	114	100.0	64	18	AA07784 Human complement C
3	114	100.0	65	18	AA07785 Human complement C
4	114	100.0	66	18	AA07786 Human complement C
5	114	100.0	67	18	AA07787 Human complement C
6	114	100.0	68	18	AA07788 Human complement C
7	114	100.0	69	18	AA07789 Human complement C
8	114	100.0	70	18	AA07790 Human complement C
9	114	100.0	71	18	AA07782 Human complement C

10	114	100.0	71	18	AA07783 Human complement C
11	114	100.0	71	18	AA07804 Human complement C
12	114	100.0	71	18	AA07791 Human complement C
13	114	100.0	72	18	AA07792 Human complement C
14	114	100.0	74	22	AA074053 Human C5a. Homo s
15	111	97.4	20	22	AA074111 C-terminal truncat
16	110	96.5	20	22	AA074110 C-terminal truncat
17	110	96.5	20	22	AA074112 C-terminal truncat
18	110	96.5	20	22	AA074113 C-terminal truncat
19	110	96.5	20	22	AA074114 C-terminal truncat
20	110	96.5	20	22	AA074116 C-terminal truncat
21	110	96.5	74	22	AA074119 Variant human C5a.
22	109	95.6	19	22	AA074097 C-terminal truncat
23	109	95.6	20	22	AA074120 Human C5a peptide
24	109	95.6	74	8	AA07166 Human anaphylatoxi
25	109	95.6	74	16	AA075497 Human C5a protein.
26	109	95.6	74	20	Solid phase sequen
27	109	95.6	74	22	AA099580 Human C5a anaphyla
28	109	95.6	74	24	ABP66209 Binding epitope of
29	109	95.6	1251	23	ABG70358 Novel human thromb
30	109	95.6	1602	23	ABG70359 Novel human thromb
31	109	95.6	1676	16	AA074107 Pro-C5 polypeptide
32	108	94.7	20	22	AA074108 C-terminal truncat
33	108	94.7	20	22	AA074115 C-terminal truncat
34	106	93.0	20	22	AA074117 C-terminal truncat
35	105	92.1	18	22	AA074098 C-terminal truncat
36	105	92.1	19	22	AA074102 C-terminal truncat
37	102	89.5	20	22	AA074109 C-terminal truncat
38	101	88.6	17	22	AA074099 C-terminal truncat
39	98	86.0	20	22	AA074117 C-terminal truncat
40	96	84.2	16	22	AA074100 C-terminal truncat
41	96	84.2	18	22	AA074103 C-terminal truncat
42	94	82.5	74	22	AA05456 Cow C5a anaphylato
43	94	82.5	74	22	AA074057 Bovine C5a. Bos s
44	93	81.6	74	22	AA05455 Pig C5a anaphylato
45	93	81.6	74	22	AA074058 Porcine C5a. Sus

## ALIGNMENTS

RESULT 1  
ID AAB74055 standard, Peptide, 20 AA.  
XX AAB74055;  
AC AAB74055;  
XX 16-MAY-2001 (first entry)  
DT 16-MAY-2001 (first entry)  
XX Human C5a peptide fragment #2.  
DE Human C5a peptide fragment #2.  
XX Human; C5a; complement; antibody; bacterial infection; sinusitis;  
KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
KW wound; anaphylatoxin; sepsis.  
XX  
OS Homo sapiens.  
XX  
PN WO200115731-A1.  
XX  
XX 08-MAR-2001.  
PD 08-MAR-2001.  
XX 31-AUG-2000; 2000WO-US24219.  
PF 31-AUG-2000; 2000WO-US24219.  
XX 31-AUG-1999; 99US-0387671.  
PR 31-AUG-1999; 99US-0387671.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
PA Ward PA, Huber-Lang M, Sarma V;  
XX  
XX WPI; 2001-22665/23.  
DR N-PSDB; AAF5793.  
XX  
XX Compositions for treating blood-borne and toxin mediated diseases and

PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PS antibodies generated against C-terminal truncated C5a peptides -  
 XX Claim 8; Page 26; 84pp; English.  
 PS  
 CC The present sequence is a peptide fragment of human complement component  
 CC C5a (the full-length sequence is given in AAB74053). The present  
 CC invention relates to an antibody specific for the present sequence. The  
 CC C5a-antibody can be used in a therapeutic composition, which is useful  
 CC for treating a subject suffering from bacterial infection, e.g.  
 CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract  
 CC infections or infections in wounds. In addition, the C5a antibody can  
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.  
 XX  
 SQ Sequence 20 AA;  
 OY  
 DB 1 CCYDASVNNDETCEQRAAR 20  
 1 CCYDASVNNDETCEQRAAR 20  
 Query Match 100.0%; Score 114; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAM07784  
 ID AAM07784 standard; protein; 64 AA.  
 AC  
 XX AAM07784;  
 XX  
 DT 01-SEP-1997 (first entry)  
 XX  
 DE Human complement C5a protein derivative analogue 1.  
 XX  
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;  
 KW treatment; prevention; disease; inflammation; pneumonia; burn;  
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;  
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;  
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;  
 KW immunosuppressive therapy; blood transfusion; dysfunction;  
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.  
 KM  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FH MISC-difference 1  
 FT MISC-difference 27 /note= "wild type Thr replaced by Met"  
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"  
 FT MISC-difference 64 /note= "wild type Asn replaced by Cys"  
 FT  
 XX  
 PN WO9639503-A1.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP02422.  
 XX  
 PR 05-JUN-1995; 95US-0463377.  
 PR 05-JUN-1995; 95US-0462648.  
 PR 05-JUN-1995; 95US-0463224.  
 XX  
 PA (CIBA ) CIBA GEIGY AG.  
 XX  
 PI Schmitz A, Van Heeke G, Van Oostrum J;  
 DR WPI; 1997-043125/04.  
 XX  
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor  
 PT antagonists, partic. for treating C5a-mediated diseases and  
 PT inflammatory conditions

XX  
 PS Example 3; Page -; 93pp; English.  
 XX  
 CC The present sequence, the human complement C5a derivative 1-64,  
 CC Thimet, Cys27Ser, Asn6Cys, is a C5a receptor antagonist which  
 CC exhibits no agonist activity. It can be used to treat or prevent  
 CC C5a mediated diseases or inflammation, e.g. pneumonia, adult  
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or  
 CC injury, post myocardial infarction inflammation, inflammatory bowel  
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,  
 CC severe trauma and burns. It can also be used to treat patients  
 CC suffering from transplant rejection, receiving immunosuppressive  
 CC therapy or massive blood transfusion, exposed to medical devices  
 CC or experiencing pulmonary dysfunction following haemodialysis or  
 CC leukopheresis. It can also be used as a prophylactic, particularly  
 CC in conditions caused by reperfusion, e.g. reperfusion following  
 CC ischaemia, and circulatory contact with medical devices, as well as  
 CC to prevent transplant rejection.  
 CC Antibodies against the derivative can be used to detect or quantify  
 CC the derivative and modify, e.g. neutralise, its activity in vivo.  
 CC N.B. Sequence not given in specification, but constructed using the  
 CC wild type sequence given on pages 51-52.  
 XX  
 SQ Sequence 64 AA;  
 OY  
 DB 1 CCYDASVNNDETCEQRAAR 20  
 21 CCYDASVNNDETCEQRAAR 40  
 Query Match 100.0%; Score 114; DB 18; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 AAM07785  
 ID AAM07785 standard; protein; 65 AA.  
 AC  
 XX AAM07785;  
 XX  
 DT 01-SEP-1997 (first entry)  
 XX  
 DE Human complement C5a protein derivative analogue 2.  
 XX  
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;  
 KW treatment; prevention; disease; inflammation; pneumonia; burn;  
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;  
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;  
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;  
 KW immunosuppressive therapy; blood transfusion; dysfunction;  
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.  
 KM  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FH MISC-difference 1 /note= "wild type Thr replaced by Met"  
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"  
 FT MISC-difference 65 /note= "wild type Ile replaced by Cys"  
 FT  
 XX  
 PN WO9639503-A1.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP02422.  
 XX  
 PR 05-JUN-1995; 95US-0463377.  
 PR 05-JUN-1995; 95US-0462648.  
 PR 05-JUN-1995; 95US-0463224.  
 XX

PA	(CIBA ) CIBA GEIGY AG.
XX	
PI	Schmitz A, Van Heeke G, Van Ooetrum J;
DR	WPI: 1997-043125/04.
XX	
PT	New human complement C5a polypeptide deriv. - used as C5a receptor
PT	antagonists, partic. for creating C5a-mediated diseases and
XX	inflammatory conditions
XX	
PS	Example 3; Page -; 93pp; English.
XX	
CC	The present sequence, the human complement C5a derivative 1-65,
CC	Thrlwct, Cys27Ser, Ile65Cys, is a C5a receptor antagonist which
CC	exhibits no agonist activity. It can be used to treat or prevent
CC	C5a mediated diseases or inflammation, e.g. pneumonitis, adult
CC	respiratory distress syndrome (ARDS), pulmonary inflammation or
CC	injury, post myocardial infarction inflammation, inflammatory bowel
CC	disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
CC	severe trauma and burns. It can also be used to treat patients
CC	suffering from transplant rejection, receiving immunosuppressive
CC	therapy or massive blood transfusion, exposed to medical devices
CC	or experiencing pulmonary dysfunction following haemodialysis or
CC	leukopheresis. It can also be used as a prophylactic, particularly
CC	in conditions caused by reperfusion, e.g. reperfusion following
CC	ischemia, and circulatory contact with medical devices, as well as
CC	to prevent transplant rejection.
CC	Antibodies against the derivative can be used to detect or modify
CC	the derivative and modify, e.g. neutralise, its activity in vivo.
CC	N.B. Sequence not given in specification, but constructed using the
CC	wild type sequence given on pages 51-52.
XX	
SQ	Sequence 65 AA:
Query Match	100.0%; Score 114; DB 18; Length 65;
Best Local Similarity	100.0%; Pred. NO. 2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CCYDGASVNDTCEORAR 20
Db	21 CCYDGASVNDTCEORAR 40
RESULT 4	
ID	AAW07786 standard; protein; 66 AA.
XX	
AC	AAW07786;
XX	
DT	01-SEP-1997 (first entry)
XX	
DE	Human complement C5a protein derivative analogue 3.
XX	
KW	Human; complement; C5a; derivative; receptor; antagonist; trauma;
KW	treatment; prevention; disease; inflammation; pneumonitis; burn;
KW	adult respiratory distress syndrome; ARDS; pulmonary injury;
KW	post myocardial infarction; inflammatory bowel; endotoxic shock;
KW	rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW	immunosuppressive therapy; blood transfusion; dysfunction;
KW	haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 1 Location/Qualifiers
FT	/note= "wild type Thr replaced by Met"
FT	27
FT	Misc-difference 27
FT	/note= "wild type Cys replaced by Ser"
FT	66
FT	Misc-difference 66
FT	/note= "wild type Ser replaced by Cys"
FN	W09639503-A1.

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XX 12-DEC-1996.
PD
XX PF 04-JUN-1996; 96MO-EP02422.
XX PR 05-JUN-1995; 95US-0463377.
PR 05-JUN-1995; 95US-0462648.
PR 05-JUN-1995; 95US-0463224.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Schmitz A, Van Heeke G, Van Oostrum J;
XX DR WPI; 1997-043125/04.
XX PT New human complement C5a polypeptide derivs. - used as C5a receptor
PT antagonists, pattic. for treating C5a-mediated diseases and
PT inflammatory conditions
XX Example 3; Page -: 93pp; English.
PS
XX The present sequence, the human complement C5a derivative 1-66,
XX ThrlMet, Cys7Ser, Ser6Gly, is a C5a receptor antagonist which
CC exhibits no agonist activity. It can be used to treat or prevent
CC C5a mediated diseases or inflammation, e.g. pneumonitis, adult
CC respiratory distress syndrome (ARDS), pulmonary inflammation or
CC injury, post myocardial infarction inflammation, inflammatory bowel
CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
CC severe trauma and burns. It can also be used to treat patients
CC suffering from transplant rejection, receiving immunosuppressive
CC therapy or massive blood transfusion, exposed to medical devices
CC or experiencing pulmonary dysfunction following haemodialysis or
CC leukopheresis. It can also be used as a prophylactic, particularly
CC in conditions caused by reperfusion, e.g. reperfusion following
CC ischaemia, and circulatory contact with medical devices, as well as
CC to prevent transplant rejection.
CC Antibodies against the derivative can be used to detect or quantify
CC the derivative and modify, e.g. neutralise, its activity in vivo.
CC N.B. Sequence not given in specification, but constructed using the
CC wild type sequence given on pages 51-52.
XX
SQ Sequence 66 AA;
Query Match 100.0%; Score 114; DB 18; Length 66;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCYGAGSYNDTCEORAR 20
Db 21 CCYGAGSYNDTCEORAR 40
|||||
|||
|
RESULT 5
AAW07787
ID AAW07787 standard; protein; 67 AA.
AC
XX AAW07787;
XX AC
XX DT 01-SEP-1997 (first entry)
XX DE Human complement C5a protein derivative analogue 4.
XX KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
KW treatment; prevention; disease; inflammation; pneumonia; burn;
KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
KW post myocardial infarction; inflammation; inflammatory bowel; endotoxemic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX OS Homo sapiens.
OS Synthetic.
XX
```

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FH Key Location/Qualifiers
FT Misc-difference 1 /note= "wild type Thr replaced by Met"
FT FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
FT FT Misc-difference 67 /note= "wild type His replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a poly-peptide derive. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -; 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-67,
XX Thrlmet, Cys27Ser, His67Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX CC Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX CC N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 67 AA;
SQ
Query Match 100.0%; Score 114; DB 18; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCYDGASVNNDETCEQRAAR 20
Db 21 CCYDGASVNNDETCEQRAAR 40

```

```

KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
KW post myocardial infarction; inflammation; inflammatory bowel; endotoxic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "wild type Thr replaced by Met"
XX FT FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
XX FT FT Misc-difference 68 /note= "wild type Lys replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a poly-peptide derive. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -; 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-68,
XX Thrlmet, Cys27Ser, Lys68Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX CC Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX CC N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 68 AA;
SQ
Query Match 100.0%; Score 114; DB 18; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCYDGASVNNDETCEQRAAR 20
Db 21 CCYDGASVNNDETCEQRAAR 40

```

```

XX AAM07789,
AC
XX 01-SEP-1997 (first entry)
DT
XX
DE Human complement C5a protein derivative analogue 6.
XX
XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX treatment; prevention; disease; inflammation; pneumonitis; burn;
XX adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX post myocardial infarction; inflammatory bowel; endotoxic shock;
XX rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
XX immunosuppressive therapy; blood transfusion; dysfunction;
XX haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
FH MISC-difference 1
FT MISC-difference 1 /note= "wild type Thr replaced by Met"
FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
FT MISC-difference 69 /note= "wild type Asp replaced by Cys"
FT MISC-difference 69 /note= "wild type Asp replaced by Cys"
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XX MO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI, 1997-043125/04.
XX
XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-69,
XX ThirMet, Cys27Ser, Asp69Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 69 AA;
XX
XX Query Match 100.0%; Score 114; DB 18; Length 69;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 CCYDGSVNNDETCEQRAAR 20
DB 21 CCYDGSVNNDETCEQRAAR 40
XX
XX RESULT 8
XX AAM07790
XX AAM07790 standard; protein; 70 AA.
XX
XX AAM07790;
XX
XX 01-SEP-1997 (first entry)
XX
XX Human complement C5a protein derivative analogue 7.
XX
XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX treatment; prevention; disease; inflammation; pneumonitis; burn;
XX adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX post myocardial infarction; inflammatory bowel; endotoxic shock;
XX rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
XX immunosuppressive therapy; blood transfusion; dysfunction;
XX haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
FH MISC-difference 1
FT MISC-difference 1 /note= "wild type Thr replaced by Met"
FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
FT MISC-difference 70 /note= "wild type Met replaced by Cys"
FT MISC-difference 70 /note= "wild type Met replaced by Cys"
XX
XX MO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI, 1997-043125/04.
XX
XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-70,
XX ThirMet, Cys27Ser, Met70Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify

```

CC the derivative and modify, e.g. neutralise, its activity in vivo.  
 CC N.B. Sequence not given in specification, but constructed using the  
 CC wild type sequence given on pages 51-52.

CC Sequence 70 AA;

Query Match 100.0%; Score 114; DB 18; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
 |||||  
 21 CCYDGASVNNDETCEORAR 40

RESULT 9  
 AAM07782  
 ID AAM07782 standard; protein; 71 AA.

XX AAM07782;

DT 01-SEP-1997 (first entry)

DE Human complement C5a protein derivative.

KM Human; complement; C5a; derivative; receptor; antagonist; trauma;  
 KM treatment; prevention; disease; inflammation; pneumonitis; burn;  
 KM adult respiratory distress syndrome; ARDS; pulmonary; injury;  
 KM post myocardial; infarction; inflammatory bowel; endotoxic shock;  
 KM rheumatoid arthritis; psoriasis; sepsis; transplant rejection;  
 KM immunosuppressive therapy; blood transfusion; dysfunction;  
 KM haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1 /note= "wild type Thr replaced by Gly"

FT Misc-difference 27 /note= "wild type Cys replaced by Ser"

FT Misc-difference 71 /note= "wild type Gln replaced by Cys"

XX WO9639503-A1.

XX 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP02422.

PR 05-JUN-1995; 95US-0463377.

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX (CIBA ) CIBA GEIGY AG.

XX Schmitz A, Van Heeke G, Van Oostrum J;

XX WPI; 1997-043125/04.

PT New human complement C5a poly-peptide derivs. - used as C5a receptor

PT antagonists, partic. for treating C5a-mediated diseases and

XX inflammatory conditions

XX Claim 11; Page -; 93pp; English.

CC The present sequence, the human complement C5a derivative 1-71,  
 CC Thr31Gly, Cys27Ser, Gln71Cys, is a C5a receptor antagonist which  
 CC exhibits no agonist activity. It can be used to treat or prevent  
 CC C5a mediated diseases or inflammation, e.g. pneumonitis, adult  
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or  
 CC injury, post myocardial infarction inflammation, inflammatory bowel  
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,

CC severe trauma and burns. It can also be used to treat patients  
 CC suffering from transplant rejection, receiving immunosuppressive  
 CC therapy or massive blood transfusion, exposed to medical devices  
 CC or experiencing pulmonary dysfunction following haemodialysis or  
 CC leukopheresis. It can also be used as a prophylactic, particularly  
 CC in conditions caused by reperfusion, e.g. reperfusion following  
 CC ischaemia, and circulatory contact with medical devices, as well as  
 CC to prevent transplant rejection.  
 CC Antibodies against the derivative can be used to detect or quantify  
 CC the derivative and modify, e.g. neutralise, its activity in vivo.  
 CC N.B. Sequence not given in specification, but constructed using the  
 CC wild type sequence given on pages 51-52.

SQ Sequence 71 AA;

Query Match 100.0%; Score 114; DB 18; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20  
 |||||  
 21 CCYDGASVNNDETCEORAR 40

RESULT 10  
 AAM07783  
 ID AAM07783 standard; protein; 71 AA.

XX AAM07783;

DT 01-SEP-1997 (first entry)

DE Human complement C5a protein derivative.

KM Human; complement; C5a; derivative; receptor; antagonist; trauma;  
 KM treatment; prevention; disease; inflammation; pneumonitis; burn;  
 KM adult respiratory distress syndrome; ARDS; pulmonary; injury;  
 KM post myocardial; infarction; inflammatory bowel; endotoxic shock;  
 KM rheumatoid arthritis; psoriasis; sepsis; transplant rejection;  
 KM immunosuppressive therapy; blood transfusion; dysfunction;  
 KM haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1 /note= "wild type Thr replaced by Gly"

FT Misc-difference 27 /note= "wild type Cys replaced by Ser"

FT Misc-difference 67 /note= "wild type His replaced by Phe"

FT Misc-difference 71 /note= "wild type Gln replaced by Cys"

XX WO9639503-A1.

XX 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP02422.

PR 05-JUN-1995; 95US-0463377.

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX (CIBA ) CIBA GEIGY AG.

XX Schmitz A, Van Heeke G, Van Oostrum J;

XX WPI; 1997-043125/04.  
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor  
 PT antagonists, partic. for treating C5a-mediated diseases and



05-JUN-1995; 95US-0463377.

```
FT      /note= "wild type cys replaced by ser"
```

```

FT Misc-difference 71
FT /note= "wild type Gln replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-71,
XX Thir1et, Cys27Ser, Gln71Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 71 AA;
XX
XX Query Match 100.0%; Score 114; DB 18; Length 71;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCYDGASVNNDETCEQRAAR 20
XX 21 CCYDGASVNNDETCEQRAAR 40
XX
XX Db
XX
XX RESULT 13
XX AAM07792
XX ID AAM07792 standard; protein; 72 AA.
XX
XX AAM07792;
XX
XX 01-SEP-1997 (first entry)
XX
XX Human complement C5a protein derivative analogue 9.
XX
XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX treatment; prevention; disease; inflammation; pneumonitis; burn;
XX adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX post myocardial; infarction; inflammatory bowel; endotoxic shock;
XX rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
XX immunosuppressive therapy; blood transfusion; dysfunction;
XX haemodialysis; leukopheresis; prophylaxis; reperfusion.

```

```

XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1
XX FT /note= "wild type Thr replaced by Met"
XX FT Misc-difference 27
XX FT /note= "wild type Cys replaced by Ser"
XX FT Misc-difference 72
XX FT /note= "wild type Leu replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-72,
XX Thir1et, Cys27Ser, Leu72Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 72 AA;
XX
XX Query Match 100.0%; Score 114; DB 18; Length 72;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCYDGASVNNDETCEQRAAR 20
XX 21 CCYDGASVNNDETCEQRAAR 40
XX
XX Db
XX
XX RESULT 14
XX AAB74053
XX ID AAB74053 standard; protein; 74 AA.
XX
XX AAB74053;
XX
XX 16-MAY-2001 (first entry)
XX

```

DE Human C5a.  
XX  
XX Human; C5a; complement; antibody; bacterial infection; sinusitis;  
KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
XX wound; anaphylatoxin; sepsis.  
OS Homo sapiens.  
XX  
XX W0200115731-A1.  
XX  
XX 08-MAR-2001.  
XX  
XX 31-AUG-2000; 2000WO-US24219.  
XX  
XX 31-AUG-1999; 99US-0387671.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
XX  
XX Ward PA, Huber-Lang M, Sarma V;  
XX  
XX WPI; 2001-226665/23.  
XX  
XX N-PSDB; AAF75791.  
XX  
XX Compositions for treating blood-borne and toxin mediated diseases and  
XX treatment of sepsis in humans and other animals comprises anti-C5a  
XX antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Example 7; Page 26; 84pp; English.  
XX  
XX The present sequence is human complement component C5a. The present  
XX invention relates to an antibody specific for the present sequence. The  
XX C5a-antibody can be used in a therapeutic composition, which is useful  
XX for treating a subject suffering from bacterial infection, e.g.  
XX sinusitis, meningitis, respiratory, gastrointestinal or urinary tract  
XX infections or infections in wounds. In addition, the C5a antibody can  
XX be used for treating sepsis. C5a is also known as anaphylatoxin.  
XX  
SQ Sequence 74 AA;  
  
Query Match 100.0%; Score 114; DB 22; Length 74;  
Best Local Similarity 100.0%; Pred. No. 2.3e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCYDGASVNNDETCEQRAAR 20  
Db 21 CCYDGASVNNDETCEQRAAR 40  
  
RESULT 15  
AAB74111  
ID AAB74111 standard; Peptide: 20 AA.  
XX  
XX AAB74111;  
XX  
XX 16-MAY-2001 (first entry)  
XX  
XX C-terminal truncated C5a peptide #49.  
XX  
XX C5a; complement; antibody; bacterial infection; sinusitis;  
KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
KW wound; anaphylatoxin; sepsis.  
XX  
XX Unidentified.  
XX  
XX W0200115731-A1.  
XX  
XX 08-MAR-2001.  
XX  
XX 31-AUG-2000; 2000WO-US24219.  
XX  
XX 31-AUG-1999; 99US-0387671.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
XX  
XX

XX  
XX Ward PA, Huber-Lang M, Sarma V;  
XX  
XX WPI; 2001-226665/23.  
XX  
XX Compositions for treating blood-borne and toxin mediated diseases and  
XX treatment of sepsis in humans and other animals comprises anti-C5a  
XX antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Page 30; 84pp; English.  
XX  
XX The present sequence is a C-terminal truncated C5a peptide fragment. The  
XX present invention relates to an antibody specific for the present  
XX sequence. The C5a-antibody can be used in a therapeutic composition,  
XX which is useful for treating a subject suffering from bacterial  
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
XX urinary tract infections or infections in wounds. In addition, the C5a  
XX antibody can be used for treating sepsis. C5a is also known as  
XX anaphylatoxin.  
XX  
SQ Sequence 20 AA;  
  
Query Match 97.4%; Score 111; DB 22; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.6e-10;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCYDGASVNNDETCEQRAAR 20  
Db 1 CCYDGATVNNDETCEQRAAR 20  
  
Search completed: December 9, 2003, 14:06:39  
Job time : 42 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 9, 2003, 14:05:43 / Search time 35 Seconds  
(without alignments)  
147.459 Million cell updates/sec

Title: US-09-651-685A-5  
Perfect score: 114  
Sequence: 1 CCYDGASVNNDETCEGPAPR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	73.7	77	11 Q63078	Q63078 ratu
2	84	73.7	742	11 Q8BNV3	Q8BNV3 mus musculu
3	81	71.1	348	11 Q8BNV9	Q8BNV9 mus musculu
4	81	71.1	352	11 Q8BWS8	Q8BWS8 mus musculu
5	56.5	49.6	1148	11 Q61372	Q61372 mus musculu
6	56.5	49.6	1738	11 Q70046	Q70046 mus musculu
7	51	44.7	608	5 Q9V174	Q9V174 dirosophila
8	50.5	44.3	1614	13 Q98977	Q98977 oncorhynch
9	49.5	43.4	483	5 Q9N497	Q9N497 caenorhabdi
10	48	42.1	135	12 Q65686	Q65686 beet necrot
11	48	42.1	282	12 Q9DGS4	Q9DGS4 beet necrot
12	48	42.1	282	12 Q9DGS5	Q9DGS5 beet necrot
13	48	42.1	282	12 Q65670	Q65670 beet necrot
14	48	42.1	282	12 Q9D567	Q9D567 beet necrot
15	48	42.1	282	12 Q9D585	Q9D585 beet necrot
16	48	42.1	282	12 Q9D575	Q9D575 beet necrot

17	47.5	41.7	1684	13 Q9DDV9	Q9DDV9 oncorhynch
18	47	41.2	227	5 Q9GT77	Q9GT77 plasmodium
19	47	41.2	834	12 Q85429	Q85429 rice stripe
20	47	41.2	834	12 Q85430	Q85430 rice stripe
21	47	41.2	1625	12 Q55597	Q55597 garlic viru
22	46	40.4	265	16 Q8XH54	Q8XH54 clostridium
23	45.5	39.9	1159	13 Q9YIA6	Q9YIA6 cyprinus ca
24	45.5	39.9	1640	13 Q9YIA8	Q9YIA8 cyprinus ca
25	45.5	39.9	1642	13 Q9YIA9	Q9YIA9 cyprinus ca
26	45.5	39.9	1642	13 Q9YIB0	Q9YIB0 cyprinus ca
27	45	39.5	141	16 Q8F117	Q8F117 escherichia
28	45	39.5	159	16 Q9CGL1	Q9CGL1 lactococcus
29	45	39.5	163	12 Q9J813	Q9J813 spodoptera
30	45	39.5	221	5 Q9NL25	Q9NL25 plasmodium
31	45	39.5	226	5 Q9N601	Q9N601 plasmodium
32	45	39.5	226	5 Q9NL21	Q9NL21 plasmodium
33	45	39.5	226	5 Q9N605	Q9N605 plasmodium
34	45	39.5	231	5 Q9N673	Q9N673 plasmodium
35	45	39.5	231	5 Q9NL20	Q9NL20 plasmodium
36	45	39.5	231	5 Q9N681	Q9N681 plasmodium
37	45	39.5	231	5 Q9NL24	Q9NL24 plasmodium
38	45	39.5	231	5 Q9NL22	Q9NL22 plasmodium
39	45	39.5	231	5 Q9NL19	Q9NL19 plasmodium
40	45	39.5	231	5 Q9NL23	Q9NL23 plasmodium
41	45	39.5	236	5 Q9NL18	Q9NL18 plasmodium
42	45	39.5	236	5 Q96556	Q96556 plasmodium
43	45	39.5	282	12 Q9D577	Q9D577 beet necrot
44	45	39.5	394	5 Q93521	Q93521 caenorhabdi
45	45	39.5	739	2 Q87381	Q87381 haemophilus

## ALIGNMENTS

## RESULT 1

Q63078 PRELIMINARY; PRT; 77 AA.  
ID Q63078;  
AC Q63078;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, last annotation update)  
DE Csa complement component protein (Fragment).  
GN CSA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lewis; TISSUE=Liver;  
RX MEDLINE=97236424; PubMed=9116048;  
RA Rothermel E., Rolf O., Goetze O., Zwirner J.;  
RT "Nucleotide and corrected amino acid sequence of the functional  
RT recombinant rat anaphylatoxin Csa.";  
RL Biochim. Biophys. Acta 1351:9-12(1997).  
DR EMBL; X91892; CAA62994.1; -;  
DR HSSP; P01031; IKJS.  
DR Interpro; IPR000020; Anaphylatoxin.  
DR Interpro; IPR001840; Anaphylatoxin.  
DR Pfam; PF01821; ANATO. 1.  
DR PRINTS; PRO00004; ANAPHYLATOXN.  
DR PRODOM; PD003264; ANAPHYLATOXIN. 1.  
DR SMART; SM00104; ANATO. 1.  
DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 1.  
FT NON\_TER 1 77  
FT NON\_TER 77 77  
SQ SEQUENCE 77 AA; 8981 MW; 14141P41CC38BD28 CRC64;  
Query Match 73.7%; Score 84; DB 11; Length 77;  
Best Local Similarity 75.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDASVNDTECEORAR 20  
DB 24 CCYDAGARNYHETCEORVAR 43

## RESULT 2

ID QB8BV3 PRELIMINARY; PRT; 742 AA.  
AC QB8BV3;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hemolytic complement (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK080166; BAC37836.1; -.  
FT NON TER 742  
SQ SEQUENCE 742 AA; 83511 MW; C730312767BA043D CRC64;

Query Match 73.7%; Score 84; DB 11; Length 742;  
Best Local Similarity 75.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCYDASVNDTECEORAR 20  
DB 702 CCYDAGARNYHETCEORVAR 721

## RESULT 3

ID QB8WN9 PRELIMINARY; PRT; 348 AA.  
AC QB8WN9;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical Anaphylotoxins.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK050413; BAC34242.1; -.  
KM Hypothetical protein.  
SQ SEQUENCE 348 AA; 39591 MW; A27D35A4D5B5E19D CRC64;

Query Match 71.1%; Score 81; DB 11; Length 348;  
Best Local Similarity 75.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDASVNDTECEORAR 20  
DB 276 CCYDAGARNYHETCEORVAR 295

## RESULT 4

ID QB8WS8 PRELIMINARY; PRT; 352 AA.  
AC QB8WS8;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical Anaphylotoxins.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK050126; BAC34079.1; -.  
KM Hypothetical protein.  
SQ SEQUENCE 352 AA; 40039 MW; 174A853E21CEFE11 CRC64;

Query Match 71.1%; Score 81; DB 11; Length 352;  
Best Local Similarity 75.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDASVNDTECEORAR 20  
DB 295 CCYDAGARNYHETCEORVAR 314

## RESULT 5

ID QB1372 PRELIMINARY; PRT; 1148 AA.  
AC QB1372;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE C4 complement protein (Fragment).  
GN C4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B10.D2(C4(h)Slp(a));  
RX MEDLINE=86176748; PubMed=3008092;  
RA Hemenway C., Kalfi M., Stavenhagen J., Walthall D., Robins D.;  
RT "Sequence comparison of alleles of the fourth component of complement  
(C4) and sex-limited protein (Slp)."  
RL Nucleic Acids Res. 14:2539-2554 (1986).  
DR EMBL; X05314; CAA28936.1; -.  
DR HSSP; P01031; 1KJS.  
DR MGD; MGI:88228; C4.  
DR InterPro; IPR002890; A2M\_N.  
DR InterPro; IPR000020; Anaphylatoxin.  
DR InterPro; IPR001840; Anaphylatoxin.  
DR InterPro; IPR001599; MacroglobulinA2.  
DR InterPro; IPR001134; Netrin\_C.  
DR Pfam; PF00207; A2M; 1.  
DR Pfam; PF01835; A2M\_N; 1.  
DR Pfam; PF01821; ANATO; 1.  
DR Pfam; PF01759; NTR; 1.  
DR PRINTS; PR00004; ANAPHYLATOXN.  
DR PRODOM; PD003264; Anaphylatoxin; 1.  
DR SMART; SM00104; ANATO; 1.  
DR SMART; SM00643; C45C; 1.  
DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.

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DR PROSITE, PS01178; ANAPHYLATOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 1148 AA; 127361 MW; 2710ECF832B6FC9 CRC64;

Query Match
Best Local Similarity 49.6%; Score 56.5; DB 11; Length 1148;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDG-ASVNDTCGEORAR 20
Db 110 CCODGMRKLPKMRICEORAR 130

RESULT 6
ID 070346 PRELIMINARY; PRT; 1738 AA.
AC 070346.
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Complement C4.
GN STR19 OR C4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas G.,
RA Hood L.;
RT "Sequence of the mouse major histocompatibility locus class III
RT region.";
RL EMBL; AF049850; AAC05279.1; -.
DR HSSP; P01031; IKOS.
DR MED; MG1:88228; C4.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001599; Macrogloblna2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01753; NTR; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR PRODOM; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
SQ SEQUENCE 1738 AA; 192944 MW; BDD2802091EE81 CRC64;

Query Match
Best Local Similarity 49.6%; Score 56.5; DB 11; Length 1738;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDG-ASVNDTCGEORAR 20
Db 700 CCODGMRKLPKMRICEORAR 720

RESULT 7
ID 09V174 PRELIMINARY; PRT; 608 AA.
AC 09V174.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE CG10055 protein.
GN CG10055.

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OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melnikov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AB003672; AAF54051.1; -.
DR FlyBase; FBgn0037482; CG10055.
DR InterPro; IPR007009; SHO1.
DR Pfam; PF04925; SHO1; 1.
SQ SEQUENCE 608 AA; 69145 MW; 035736E5F267014 CRC64;

Query Match
Best Local Similarity 44.7%; Score 51; DB 5; Length 608;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CYDGASVNDTCGE 15
Db 327 CYDVRTNNPTCE 340

RESULT 8
ID 098977 PRELIMINARY; PRT; 1614 AA.
AC 098977.
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Complement component C3-3 (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei.

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OC Protactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96323260; PubMed=8710907;
RA Sunyer J.O., Zarkadis I.K., Sahu A., Lambiris J.D.;
RT "Multiple forms of complement C3 in trout that differ in binding to
  complement activators.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:8546-8551(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20437839; PubMed=10960316;
RA Zarkadis I.K., Satrias M.R., Styroera G., Sunyer J.O., Lambiris J.D.;
RT "Cloning and structure of three rainbow trout C3 molecules: a
  plausible explanation for their functional diversity.";
RL Dev. Comp. Immunol. 25:11-24(2001).
DR EMBL; U61753; AAC60015.2; -.
DR HSP; P01024; ICD3.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001599; MacroglobulinA2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR PRINTS; PRO0004; ANAPHYLATOXN.
DR PRODOM; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C3A5C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 1614 AA, 180714 MW, 0910CE3B73D38F10 CRC64;

Query Match 44.3%; Score 50.5; DB 13; Length 1614;
Best Local Similarity 57.9%; Pred. No. 16;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 CCYDGASVN-NDTCEGPA 18
Db 640 CCMDGMRKNILDYTCERRA 658

RESULT 9
Q9N497 PRELIMINARY; PRT; 483 AA.
AC Q9N497;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein Y110A2AL.2.
GN Y110A2AL.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermata; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "genome sequence of the nematode C. elegans: a platform for
  investigating biology. the C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smith A.;

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RT "The sequence of C. elegans cosmid Y110A2AL.";
RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024746; AAF60400.2; -.
KW Hypothetical protein.
SQ SEQUENCE 483 AA, 52777 MW, 6633184625D9B360 CRC64;

Query Match 43.4%; Score 49.5; DB 5; Length 483;
Best Local Similarity 47.4%; Pred. No. 6.3;
Matches 9; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 1 CC-----YDGASVNDTCE 14
Db 133 CCAKRDVFDGSSSNRET 151

RESULT 10
Q65686 PRELIMINARY; PRT; 135 AA.
AC Q65686;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 15.0 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F2;
RA Bouzouba S., Guille H., Jonard G., Richards K., Putz C.;
RT "nucleotide sequence analysis of rna-3 and rna-4 of beet necrotic
  yellow vein virus, isolates f2 and g1.";
RL J. Gen. Virol. 66:1553-1564(1985).
DR EMBL; M36896; AAA69656.1; -.
DR InterPro; IPR007004; DUF656.
DR Pfam; PF04920; DUF656; 1.
KW Hypothetical protein.
SQ SEQUENCE 135 AA, 15027 MW, 79E2231BA5240226 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 135;
Best Local Similarity 57.1%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVNDTCE 15
Db 115 CYSGVDVLSDELCE 128

RESULT 11
Q9DGS4 PRELIMINARY; PRT; 282 AA.
AC Q9DGS4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 32.1 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F75, and F72;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennerts B.L.;
RT "Molecular analyses of European A. B and P type sources of Beet
  necrotic yellow vein virus and detection of the rate P type in
  Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).

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DR EMBL; AF197548; AAG37084.1; -;  
 DR EMBL; AF197546; AAG37078.1; -;  
 DR InterPro; IPR007004; DUF656.  
 DR Pfam; PF04920; DUF656; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 282 AA; 3203 MW; F8DB465FBC6B5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 6.4;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 CYDGASVNNDETCE 15  
 ||| :|||  
 Db 115 CYSGVDVLSDELCE 128

## RESULT 12

O9DS5 PRELIMINARY; PRT; 282 AA.

AC O9DS5;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 32.1 kDa protein.  
 OS Beet necrotic yellow vein virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.  
 OX NCBI\_TaxID=31721;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Kas3, and Kas2;  
 RX MEDLINE=20456802; PubMed=11003469;  
 RA Koenig R., Lemefors B.L.;  
 RT "Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan."  
 RT Arch. Virol. 145:1561-1570(2000).  
 RL EMBL; AF197557; AAG37097.1; -;  
 DR EMBL; AF197554; AAG37090.1; -;  
 DR InterPro; IPR007004; DUF656.  
 DR Pfam; PF04920; DUF656; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 282 AA; 3211 MW; F8D90D3208FB5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 6.4;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 CYDGASVNNDETCE 15  
 ||| :|||  
 Db 115 CYSGVDVLSDELCE 128

## RESULT 13

O65670 PRELIMINARY; PRT; 282 AA.

AC O65670;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE 31k protein.  
 OS Beet necrotic yellow vein virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.  
 OX NCBI\_TaxID=31721;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=S.  
 RX MEDLINE=97128991; PubMed=8973531;  
 RA Saito M., Kiguchi T., Kusume T., Tamada T.;  
 RT "Complete nucleotide sequence of the Japanese isolate S of beet necrotic yellow vein virus RNA and comparison with European isolates."  
 RT Arch. Virol. 141:2163-2175(1996).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C;  
 RA Yu J., Han C., Yang L., Li D., Liu Y.;  
 RT "cDNA cloning, sequencing and expression of RNA4 from beet necrotic yellow vein virus."  
 RT Acta Microbiol. Sin. 37:7-14(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C;  
 RA Li D.;  
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; D84413; BAA12347.1; -;  
 DR EMBL; AJ239199; CAI5427.1; -;  
 DR InterPro; IPR007004; DUF656.  
 DR Pfam; PF04920; DUF656; 1.  
 SQ SEQUENCE 282 AA; 31970 MW; D96AA3B079E063E6 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 6.4;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 CYDGASVNNDETCE 15  
 ||| :|||  
 Db 115 CYSGVDVLSDELCE 128

## RESULT 14

O9DS67 PRELIMINARY; PRT; 282 AA.

AC O9DS67;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 31.9 kDa protein.  
 OS Beet necrotic yellow vein virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.  
 OX NCBI\_TaxID=31721;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N7;  
 RX MEDLINE=20456802; PubMed=11003469;  
 RA Koenig R., Lemefors B.L.;  
 RT "Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan."  
 RT Arch. Virol. 145:1561-1570(2000).  
 RL EMBL; AF197559; AAG37099.1; -;  
 DR EMBL; AF197559; AAG37099.1; -;  
 DR InterPro; IPR007004; DUF656.  
 DR Pfam; PF04920; DUF656; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 282 AA; 31948 MW; 58A34878C868131F CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 6.4;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 CYDGASVNNDETCE 15  
 ||| :|||  
 Db 115 CYSGVDVLSDELCE 128

## RESULT 15

O9DS85 PRELIMINARY; PRT; 282 AA.

AC O9DS85;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 31.9 kDa protein.  
 OS Beet necrotic yellow vein virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.  
 OX NCBI\_TaxID=31721;  
 RN [1]



RP SEQUENCE FROM N.A.  
RC STRAIN=D71;  
RX MEDLINE=20456802; PubMed=11003469;  
RA Koenig R., Lennetors B.L.;  
RT "Molecular analyses of European A, B and P type sources of Beet  
RT necrotic yellow vein virus and detection of the rare P type in  
RT Kazakhstan."  
RL Arch. Virol. 145:1561-1570(2000).  
DR EMBL; AF197544; AAC37076.1; -.  
DR InterPro; IPR07004; DUF656.  
DR Pfam; PF04920; DUF656; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 282 AA; 31939 MW; 3383394A3A739F2D CRC64;  
  
Query Match 42.1%; Score 48; DB 12; Length 282;  
Best Local Similarity 57.1%; Pred. No. 6.4;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 CYDGASVNNDETCE 15  
||| |:  
Db 115 CYSGVDVLSDELCE 128

Search completed: December 9, 2003, 14:07:28  
Job time : 37 secs

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 9, 2003, 14:05:43 ; Search time 11 Seconds  
(without alignments)  
85,503 Million cell updates/sec

Title: US-09-651-685a-5

Perfect score: 114  
Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	109	95.6	1676	1	CO5_HUMAN
2	94	82.5	74	1	CO5A_BOVIN
3	93	81.6	74	1	CO5A_PIG
4	84	73.7	76	1	CO5A_RAT
5	84	73.7	1680	1	CO5_MOUSE
6	56.5	49.6	1738	1	CO4_MOUSE
7	55.5	48.7	920	1	CO4_BOVIN
8	55.5	48.7	1737	1	CO4_RAT
9	51.5	45.2	1744	1	CO4_HUMAN
10	48	42.1	282	1	Y32K_BNYVG
11	46	40.4	1473	1	OVO8_CHICK
12	44.5	39.0	281	1	Y125_MYCPN
13	44.5	39.0	685	1	CPAH_BOVIN
14	44.5	39.0	1249	1	UN36_CABEL
15	44	38.6	624	1	ARLY_VIBPA
16	44	38.6	624	1	ARLY_VIBPA
17	44	38.6	715	1	SL41_HUMAN
18	44	38.6	2095	1	RREP_TOSV
19	43.5	38.2	1651	1	CO3_NAUNA
20	43	37.7	337	1	DN07_CABEL
21	43	37.7	461	1	SYC_YERPE
22	42.5	37.3	705	1	FBLI_MOUSE
23	42.5	37.3	1640	1	CO3_ONCMY
24	42.5	37.3	1673	1	CO3_LAMTA
25	42	36.8	241	1	TSN1_HUMAN
26	42	36.8	261	1	RFA4_HUMAN
27	42	36.8	263	1	PSJ3_HUMAN
28	42	36.8	760	1	AD25_MOUSE
29	42	36.8	1068	1	YCF0_MARPO
30	42	36.8	2149	1	RREP_RUFVZ
31	41.5	36.4	65	1	MT_PARIT
32	41.5	36.4	486	1	MTN3_HUMAN
33	36.0	33.2	1	1	KC2A_MAIZE

34	41	36.0	450	1	VD10_BPT5
35	41	36.0	491	1	Y084_MYCTU
36	41	36.0	735	1	AD02_MACFA
37	41	36.0	1826	1	SUS1_PABIT
38	41	36.0	2230	1	GOG4_HUMAN
39	41	36.0	4543	1	LRP1_CHICK
40	41	36.0	4660	1	LRP2_RAT
41	40	35.1	351	1	Y4V7_RHISN
42	40	35.1	366	1	YGDE_ECOLI
43	40	35.1	448	1	EXG1_YEAST
44	40	35.1	448	1	GIAN_DROME
45	40	35.1	503	1	AMPA_RHILLO

## ALIGNMENTS

RESULT 1  
ID COS\_HUMAN STANDARD; PRT; 1676 AA.  
AC P01031;  
DT 21-UTL-1986 (Rel. 01, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Complement C5 precursor [Contains: C5a anaphylatoxin].  
GN C5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91079575; PubMed=1984448;  
RA Haviland D.L., Haviland J.C., Fleischner D.T., Hunt A., Wetzel R.A.;  
RT "Complete cDNA sequence of human complement pro-C5. Evidence of  
RT truncated transcripts derived from a single copy gene.";  
RL J. Immunol. 146:362-368(1991).  
RN [2]  
RP SEQUENCE OF 412-1676 FROM N.A.  
RX MEDLINE=88209511; PubMed=3365401;  
RA Wetzel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,  
RA Tack B.F.;  
RT "Molecular analysis of human complement component C5: localization of  
RT the structural gene to chromosome 9.";  
RL Biochemistry 27:1474-1482(1988).  
RN [3]  
RP SEQUENCE OF 412-902 FROM N.A.  
RX MEDLINE=85130937; PubMed=2579066;  
RA Lundwall A.B., Wetzel R.A., Kristensen T., Whitehead A.S.;  
RA Woods D.E., Ogden R.C., Colten H.R., Tack B.F.;  
RT "Isolation and sequence analysis of a cDNA clone encoding the fifth  
RT complement component.";  
RL J. Biol. Chem. 260:2108-2112(1985).  
RN [4]  
RP SEQUENCE OF 678-751.  
RX MEDLINE=79055687; PubMed=690134;  
RA Fernandez H.N., Hugli T.E.;  
RT "Primary structural analysis of the polypeptide portion of human C5a  
RT anaphylatoxin. Polypeptide sequence determination and assignment of  
RT the oligosaccharide attachment site in C5a.";  
RL J. Biol. Chem. 253:6955-6964(1978).  
RN [5]  
RP SEQUENCE OF 678-751 FROM N.A.  
RX MEDLINE=91144547; PubMed=1996961;  
RA Bohnsack J.F., Mollison K.W., Buko A.M., Ashworth J.C., Hill H.R.;  
RT "Group B streptococci inactivate complement component C5a by enzymic  
RT cleavage at the C-terminus.";  
RL Biochem. J. 273:635-640(1991).  
RN [6]  
RP STRUCTURE BY NMR OF CSA.  
RX MEDLINE=88309754; PubMed=3408713;  
RA Zuilkerer E.R.P., Mollison K.W., Henkin J., Carter G.W.;  
RT "Sequence-specific assignments in the 1H NMR spectrum of the human

RT inflammatory protein C5a.";  
 RL Biochemistry 27:3568-3580(1988).  
 RN [7]  
 RP STRUCTURE BY NMR OF C5A.  
 RX MEDLINE=89207527; PubMed=2784981;  
 RA Zuideweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.;  
 RT "tertiary structure of human complement component C5a in solution  
 from nuclear magnetic resonance data.";  
 RL Biochemistry 28:172-185(1989).  
 RN [8]  
 RP STRUCTURE BY NMR OF C5A.  
 RX MEDLINE=89274164; PubMed=2730871;  
 RA Zuideweg E.R.P., Resik S.W.;  
 RT "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory  
 protein C5a.";  
 RL Biochemistry 28:2387-2391(1989).  
 RN [9]  
 RP STRUCTURE BY NMR OF C5A.  
 RX MEDLINE=97160477; PubMed=9007977;  
 RA Zhang X., Boyar W., Galakatos N., Gonnella N.C.;  
 RT "Solution structure of a unique C5a semi-synthetic antagonist:  
 implications in receptor binding.";  
 RL Protein Sci. 6:65-72(1997).  
 RN [10]  
 RP STRUCTURE BY NMR OF C5A.  
 RX MEDLINE=97332508; PubMed=9188742;  
 RA Zhang X., Boyar W., Toch M.D., Wennogle L., Gonnella N.C.;  
 RT "Structural definition of the C5a C terminus by two-dimensional  
 nuclear magnetic resonance spectroscopy.";  
 RL Proteins 28:261-267(1997).  
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE  
 SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,  
 INTO THE MEMBRANE ATTACK COMPLEX. CSB HAS A TRANSPARENT BINDING SITE  
 FOR C6. THE CSB-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC  
 COMPLEX IS ASSEMBLED.  
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,  
 C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT  
 INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR  
 PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND  
 BASOPHILIC LEUCOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF  
 POLYMORPHONUCLEAR LEUCOCYTES (CHEMOKINESIS) AND DIRECT THEIR  
 MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).  
 CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC  
 RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE  
 BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,  
 RELEASING C5A ANAPHYLATOXIN & GENERATING CSB (BETA CHAIN + ALPHA  
 CHAIN).  
 CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.  
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855  
 ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M57729; AAA51925.1; -;  
 DR EMBL; M65134; AAA51856.1; -;  
 DR PIR; A40075; CSHU.  
 DR PDB; 1KJ5; 15-MAY-97.  
 DR PDB; 1CFA; 17-SEP-97.  
 DR Genew; HGNC:1331; C5.  
 DR MTM; 120900.  
 DR GO; GO:0005615; Extracellular space; TAS.  
 DR GO; GO:0003797; F:antibacterial peptide activity; TAS.  
 DR GO; GO:0008009; F:chemokine activity; TAS.  
 DR GO; GO:0005102; F:receptor binding activity; TAS.  
 DR GO; GO:000187; P:activation of MAPK; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalling. . .; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0009618; P:response to pathogenic bacteria; TAS.  
 DR GO; GO:0006950; P:response to stress; TAS.  
 DR InterPro; IPR002890; A2M N.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR001599; Macroglobin2.  
 DR InterPro; IPR001134; Netrin\_C.  
 DR Pfam; PF00207; A2M; 1.  
 DR Pfam; PF01835; A2M N; 1.  
 DR Pfam; PF01821; ANATO; 1.  
 DR Pfam; PF01759; NTR; 1.  
 DR ProDom; PD003264; Anaphylatoxin; 1.  
 DR SMART; SM00104; ANATO; 1.  
 DR SMART; SM00643; C3a5C; 1.  
 DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; FALSE\_NEG.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 1.  
 KW Complement pathway; Complement alternate pathway; Glycoprotein;  
 KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;  
 KW Signal; Polymorphism; 3d-structure.  
 FT SIGNAL 1 18  
 FT CHAIN 19 673  
 FT PROSERP 674 677  
 FT CHAIN 678 1676  
 FT PEPTIDE 678 751  
 FT CHAIN 752 1676  
 FT DOMAIN 698 732  
 FT DISULFID 698 724  
 FT DISULFID 699 721  
 FT DISULFID 711 732  
 FT CARBOHYD 741 741  
 FT CARBOHYD 911 911  
 FT CARBOHYD 1115 1115  
 FT CARBOHYD 1630 1630  
 FT VARIANT 518 518  
 FT VARIANT 802 802  
 FT VARIANT 1053 1053  
 FT VARIANT 1310 1310  
 FT VARIANT 1437 1437  
 FT TURN 679 680  
 FT HELIX 682 688  
 FT TURN 689 689  
 FT HELIX 693 703  
 FT TURN 704 704  
 FT HELIX 711 715  
 FT TURN 716 716  
 FT HELIX 722 739  
 FT HELIX 745 748  
 FT TURN 749 750  
 SQ SEQUENCE 1676 AA; 188331 MW; 87DCAA65FF977D19 CRC64;  
 Query Match 95.6%; Score 109; DB 1; Length 1676;  
 Best Local Similarity 95.0%; Pred No. 2.8e-09;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CCYDGA5VNNDETCEGRAR 20  
 Db 698 CCYDGA5VNNDETCEGRAR 717  
 RESULT 2  
 ID COSA BOVIN STANDARD; PRT; 74 AA.  
 AC P12082;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Complement C5A anaphylatoxin.  
 GN C5.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP MEDLINE=86136134; PubMed=3081348;  
 RX Gennaro R., Simonic T., Negri A., Motcola C., Secchi C., Ronchi S.,  
 RA Romeo D.;  
 RT "C5a fragment of bovine complement. Purification, bioassays,  
 RT amino-acid sequence and other structural studies.";  
 RL Eur. J. Biochem. 155:77-86(1986).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=89005703; PubMed=3262536;  
 RA Zarbock J., Gennaro R., Romeo D., Clore G.M., Gronenborn A.M.;  
 RT "A proton nuclear magnetic resonance study of the conformation of  
 RT bovine anaphylatoxin C5a in solution."  
 RL FEBS Lett. 238:289-294(1988).  
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,  
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT  
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR  
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND  
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF  
 CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR  
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).  
 CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.  
 CC PIR; A25408; A25408.  
 DR HSP; P01032; 1CSA.  
 DR InterPro; IPR0000020; Anaphylatoxin.  
 DR InterPro; IPR001840; Anaphylatoxin.  
 DR InterPro; IPR001599; Macroglobulin2.  
 DR Pfam; PF01821; ANATO; 1.  
 DR PRINTS; PR00004; ANAPHYLATOXN.  
 DR ProDom; PD003264; Anaphylatoxin; 1.  
 DR SMART; SM00104; ANATO; 1.  
 DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; PARTIAL.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 1.  
 DR Complement pathway; Complement alternate pathway; Plasma;  
 KW Inflammatory response.  
 KM Inflammatory response.  
 FT DOMAIN 21 55 ANAPHYLATOXIN-LIKE.  
 FT DISULFID 21 47 BY SIMILARITY.  
 FT DISULFID 22 54 BY SIMILARITY.  
 FT DISULFID 34 55 BY SIMILARITY.  
 SQ SEQUENCE 74 AA; 8517 MW; C09DPF742D12D70F6 CRC64;  
 QY 1 CCYDGA5VNNDETCERRAR 20  
 Db 21 CCYDGA5VNNDETCERRAR 40  
 Query Match 82.5%; Score 94; DB 1; Length 74;  
 Best Local Similarity 80.0%; Pred. No. 2,4e-08;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 3  
 COSA\_PIG  
 ID COSA\_PIG STANDARD; PRT; 74 AA.  
 AC P01032;  
 DT 21-UTL-1986 (Rel. 01, Created)  
 DT 21-UTL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Complement C5A anaphylatoxin.  
 GN C5.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae;  
 OX NCBI\_TaxID=9823;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=80182137; PubMed=7372604;  
 RA Gerard C., Hugli T.E.;  
 RT "Amino acid sequence of the anaphylatoxin from the fifth component of  
 RT porcine complement.";  
 RL J. Biol. Chem. 255:4710-4715(1980).  
 RN [2]  
 RP ACTIVE REGION.  
 RX MEDLINE=81195449; PubMed=6940191;  
 RA Gerard C., Hugli T.E.;  
 RT "Identification of classical anaphylatoxin as the des-Arg form of the  
 RT C5a molecule: evidence of a modulator role for the oligosaccharide  
 RT unit in human des-Arg4-C5a";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:1833-1837(1981).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=90248365; PubMed=2337573;  
 RA Williamson M.P., Madison V.S.;  
 RT "Three-dimensional structure of porcine C5adesArg from 1H nuclear  
 RT magnetic resonance data.";  
 RL Biochemistry 29:2895-2905(1990).  
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,  
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT  
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR  
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND  
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF  
 CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR  
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).  
 CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.  
 CC PDB; 1CSA; 15-OCT-91.  
 DR InterPro; IPR0000020; Anaphylatoxin.  
 DR InterPro; IPR001599; Macroglobulin2.  
 DR Pfam; PF01821; ANATO; 1.  
 DR ProDom; PD003264; Anaphylatoxin; 1.  
 DR SMART; SM00104; ANATO; 1.  
 DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; PARTIAL.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 1.  
 DR Complement pathway; Complement alternate pathway; Plasma;  
 KW Inflammatory response; 3D-structure.  
 FT DOMAIN 21 55 ANAPHYLATOXIN-LIKE.  
 FT DISULFID 21 47  
 FT DISULFID 22 54  
 FT DISULFID 34 55  
 FT SITE 72 74  
 FT HELIX 2 11  
 FT TURN 13 14  
 FT HELIX 16 26  
 FT HELIX 34 40  
 FT HELIX 45 62  
 FT TURN 63 64  
 SQ SEQUENCE 74 AA; 8609 MW; 11AFA2E94A026EB3 CRC64;  
 QY 1 CCYDGA5VNNDETCERRAR 20  
 Db 21 CCYDGA5VNNDETCERRAR 40  
 Query Match 81.6%; Score 93; DB 1; Length 74;  
 Best Local Similarity 80.0%; Pred. No. 3,5e-08;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 4  
 COSA\_RAT  
 ID COSA\_RAT STANDARD; PRT; 76 AA.  
 AC P08650;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Complement C5A anaphylatoxin.  
 GN C5.

```
OS Rattus norvegicus (Rat).
OC Bukayocia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RA Cui L.-X., Ferreri K., Hugli T.E.;
RT "Characterization of rat C5a, a uniquely active spasmogen.";
RL Complement 2:18-19(1985).
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC DR HSSP; P01031; IKJS.
CC DR InterPro; IPR000020; Anaphylatoxin.
CC DR InterPro; IPR001599; MacroglobinA2.
CC DR Pfam; PF01821; ANATO; 1.
CC DR ProDom; PD003264; Anaphylatoxin; 1.
CC DR SMART; SM00104; ANATO; 1.
CC DR PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; PARTIAL.
CC DR PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
CC DR PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
CC DR Complement pathway; Complement alternate pathway; Glycoprotein;
CC Plasma; Inflammatory response.
CC KW DOMAIN 24 58 ANAPHYLATOXIN-LIKE.
CC FT DISULFID 24 50 BY SIMILARITY.
CC FT DISULFID 25 57 BY SIMILARITY.
CC FT DISULFID 37 58 BY SIMILARITY.
CC FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .).
CC FT SEQUENCE 76 AA; 8869 MW; 2EC15183A6E54769 CRC64;
QY 1 CCYDGASVNDTECEORAR 20
Db 24 CCYDGARENKYECEORVAR 43
Query Match 73.7%; Score 84; DB 1; Length 76;
Best Local Similarity 75.0%; Pred. No. 9.8e-07;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
RESULT 5
ID COS_MOUSE STANDARD; PRT; 1680 AA.
AC P06684;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C5 precursor (Hemolytic complement) [contains: C5A
DE anaphylatoxin].
GN C5 OR HC.
OS Mus musculus (Mouse).
OC Bukayocia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90153853; PubMed=2303408;
RA Wetzel R.A., Fleischer D.T., Haviland D.L.;
RT "Deficiency of the murine fifth complement component (C5). A 2-base
RT pair gene deletion in a 5'-exon.";
RL J. Biol. Chem. 265:2435-2440(1990).
RN [2]
RP SEQUENCE OF 41-1680 FROM N.A.
RX MEDLINE=87185363; PubMed=2436653;
RX Wetzel R.A., Ogata R.T., Tack B.F.;
RT "Primary structure of the fifth component of murine complement.";
RL Biochemistry 26:737-743(1987).
CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
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CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC
CC COMPLEX IS ASSEMBLED.
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN.
CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
CC CHAIN).
CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; M35525; AAA37349.1; -.
CC DR EMBL; M35526; AAA37348.1; -.
CC DR PIR; A35530; CSM5.
CC DR HSSP; P01031; IKJS.
CC DR MGD; MG196031; HC.
CC DR InterPro; IPR002890; A2M N.
CC DR InterPro; IPR000020; Anaphylatoxin.
CC DR InterPro; IPR001840; Anaphylatoxin.
CC DR InterPro; IPR001599; MacroglobinA2.
CC DR InterPro; IPR001134; Netrin_C.
CC DR Pfam; PF00207; A2M; 1.
CC DR Pfam; PF01835; A2M N; 1.
CC DR Pfam; PF01821; ANATO; 1.
CC DR Pfam; PF01759; NTR; 1.
CC DR PRINTS; PR000004; ANAPHYLATOXN.
CC DR ProDom; PD003264; Anaphylatoxin; 1.
CC DR SMART; SM00104; ANATO; 1.
CC DR PROSITE; PS00643; C34SC; 1.
CC DR PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; FALSE_NEG.
CC DR PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
CC DR PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
CC KW Complement pathway; Complement alternate pathway; Glycoprotein;
CC Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
CC Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 1680 COMPLEMENT C5.
CC FT CHAIN 19 674 COMPLEMENT C5 BETA CHAIN.
CC FT PROPEP 675 678
CC FT CHAIN 679 1680 COMPLEMENT C5 ALPHA CHAIN.
CC FT PEPTIDE 679 755 CSA ANAPHYLATOXIN.
CC FT CHAIN 756 1680 CSB (ALPHA').
CC FT DOMAIN 702 736 ANAPHYLATOXIN-LIKE.
CC FT DISULFID 702 736 BY SIMILARITY.
CC FT DISULFID 703 735 BY SIMILARITY.
CC FT DISULFID 715 736 BY SIMILARITY.
CC FT CARBOHYD 427 427 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 915 915 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 1119 1119 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 1633 1633 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARIANT 216 216 Y -> I (IN DEFECTIVE VARIANT CSD).
CC FT VARIANT 217 1680 MISSING (IN DEFECTIVE VARIANT CSD).
CC FT SEQUENCE 1680 AA; 188877 MW; 81B5A15FAC7D95C CRC64;
QY Query Match 73.7%; Score 84; DB 1; Length 1680;
Best Local Similarity 75.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 CCYDASVNDTCORAR 20  
 DB 702 CCYDARVNFYETCERVAR 721

RESULT 6  
 C04 MOUSE STANDARD; PRT: 1738 AA.

AC P01029; 061859;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Complement C4 precursor [contains: C4A anaphylatoxin].  
 GN C4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85298264; PubMed=3862104;  
 RA Sepich D.S., Noonan D.U., Ogata R.T.;  
 RT "Complete cDNA sequence of the fourth component of murine  
 complement.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5895-5899(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=B12.WR;  
 MEDLINE=87309760; PubMed=3624865;  
 RA Rosa P.A., Sepich D.S., Robins D.M., Ogata R.T.;  
 RT "Constitutive expression of S1p genes in mouse strain B10.WR directed  
 by C4 regulatory sequences.";  
 RN J. Immunol. 139:1568-1577(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=B12.WR; TISSUE=Liver;  
 MEDLINE=89380278; PubMed=2777798;  
 RA Ogata R.T., Rosa P.A., Zepf N.E.;  
 RT "Sequence of the gene for murine complement component C4.";  
 RL J. Biol. Chem. 264:16565-16572(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=FW; TISSUE=Liver;  
 MEDLINE=85289294; PubMed=2993295;  
 RA Nonaka M., Nakayama K., Yeul Y.D., Takahashi M.;  
 RT "Complete nucleotide and derived amino acid sequences of the fourth  
 component of mouse complement (C4). Evolutionary aspects.";  
 RN J. Biol. Chem. 260:10936-10943(1985).  
 RN [5]  
 RP SEQUENCE OF 651-810 AND 924-1083 FROM N.A.  
 RX MEDLINE=85038607; PubMed=6208559;  
 RA Nonaka M., Takahashi M., Natsunne-Sakai S., Nonaka M., Tanaka S.,  
 Shimizu A., Honjo T.;  
 RT "Isolation of cDNA clones specifying the fourth component of mouse  
 complement and its isolated, sex-limited protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6822-6826(1984).  
 RN [6]  
 RP SEQUENCE OF 1099-1142 FROM N.A.  
 RX STRAIN=B10.WR, C57BL/6, C3H/He, CBA/J, B10.BR, and DBA2;  
 MEDLINE=90353398; PubMed=2387317;  
 RA Ogata R.T., Zepf N.E.;  
 RT "C4 from C4-high and C4-low mouse strains have identical sequences in  
 the region corresponding to the isotype-specific segment of human  
 C4.";  
 RL Eur. J. Immunol. 20:1607-1610(1990).  
 RN [7]  
 RP SEQUENCE OF 1105-1449 FROM N.A.  
 RX MEDLINE=85166208; PubMed=385685;  
 RA Levi-Strauss M., Tosi M., Steinmetz M., Klein J., Neo T.;  
 RT "Multiple duplications of complement C4 gene correlate with H-2-  
 controlled testosterone-independent expression of its sex-limited  
 isoform, C4-S1p.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1746-1750(1985).

RN [8]  
 RP SEQUENCE OF 1257-1376 FROM N.A.  
 RX MEDLINE=85038859; PubMed=6149581;  
 RA Tosi M., Levi-Strauss M., Duponchel C., Neo T.;  
 RT "Sequence heterogeneity of murine complementary DNA clones related to  
 the C4 and C4-S1p isoforms of the fourth complement component.";  
 RL Philoe. Trans. R. Soc. Lond., B, Biol. Sci. 306:389-394(1984).  
 RN [9]  
 RP SEQUENCE OF 1360-1511 FROM N.A.  
 RX MEDLINE=83273751; PubMed=6192448;  
 RA Ogata R.T., Shreffler D.C., Sepich D.S., Lilly S.P.;  
 RT "cDNA clone spanning the alpha-gamma subunit junction in the  
 precursor of the murine fourth complement component (C4).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5061-5065(1983).  
 RN [10]  
 RP SEQUENCE OF 1-128 FROM N.A.  
 RX STRAIN=FW; TISSUE=Liver;  
 MEDLINE=86031969; PubMed=2997024;  
 RA Nonaka M., Nakayama K., Yeul Y.D., Shimizu A., Takahashi M.;  
 RT "Molecular cloning and characterization of complementary and genomic  
 DNA clones for mouse C4 and S1p.";  
 RN Immunol. Rev. 87:81-99(1985).  
 RN [11]  
 RP SEQUENCE OF 1-21 FROM N.A.  
 RX MEDLINE=87017050; PubMed=3464002;  
 RA Nonaka M., Kimura H., Yeul Y.D., Yokoyama S., Nakayama K.,  
 Takahashi M.;  
 RT "Identification of the 5'-flanking regulatory region responsible for  
 the difference in transcriptional control between mouse complement C4  
 and S1p genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:7883-7887(1986).  
 CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE  
 CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY  
 ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A  
 ANAPHYLATOXIN  
 CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR  
 AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER  
 OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).  
 CC -1- MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III  
 PROTEIN.  
 CC -1- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.  
 CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.  
 CC -----  
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 CC -----  
 DR EMBL; K00019; AAA39554.1; -  
 DR EMBL; M11729; AAA39506.1; -  
 DR EMBL; M12968; AAA39558.1; -  
 DR EMBL; M12970; AAA39555.1; -  
 DR EMBL; M12972; AAA39556.1; -  
 DR EMBL; M12969; AAA39559.1; -  
 DR EMBL; M11789; AAA39557.1; -  
 DR EMBL; K02798; AAC42021.1; -  
 DR EMBL; M17440; AAA39561.1; -  
 DR EMBL; M14225; AAA39563.1; -  
 DR EMBL; M14226; AAA39684.1; -  
 DR EMBL; X55493; CAA39112.1; -  
 DR EMBL; X55495; CAA39114.1; -  
 DR PIR; A24558; A24558.  
 DR PIR; A28176; A28176.  
 DR HSP; P01031; IKUS.  
 DR MGJ; MGJ:88228; C4.  
 DR InterPro; IPR002890; A2M N.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR001599; MacroglobinA2.  
 DR InterPro; IPR001134; Netrin\_C.  
 DR Pfam; PF00207; A2M; 1.

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DR Pfam; PF01835; A2M N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR Complement pathway; Plasma; Glycoprotein; Sulfation; Signal;
  Inflammatory response; Thioester bond.
FT SIGNAL 1 19
FT CHAIN 20 673 COMPLEMENT C4, BETA CHAIN.
FT PROPEP 674 677
FT CHAIN 678 1443 COMPLEMENT C4, ALPHA CHAIN.
FT PROPEP 1444 1447
FT CHAIN 1448 1738 COMPLEMENT C4, GAMMA CHAIN.
FT PEPTIDE 678 753 C4A ANAPHYLATOXIN.
FT DOMAIN 700 734 ANAPHYLATOXIN-LIKE.
FT DISULFID 700 726
FT DISULFID 701 733
FT DISULFID 714 734
FT CROSSLINK 1006 1009
FT MOD_RES 1413 1413
FT MOD_RES 1416 1416
FT MOD_RES 1417 1417
FT CARBOHYD 224 224
FT CARBOHYD 743 743
FT CARBOHYD 1387 1387
FT CONFLICT 132 132
FT CONFLICT 327 327
FT CONFLICT 570 570
FT CONFLICT 720 720
FT CONFLICT 739 740
FT CONFLICT 838 838
FT CONFLICT 993 993
FT CONFLICT 1043 1043
FT CONFLICT 1119 1119
FT CONFLICT 1190 1190
FT CONFLICT 1324 1324
FT CONFLICT 1401 1401
FT CONFLICT 1442 1442
FT CONFLICT 1453 1453
SQ SEQUENCE 1738 AA; 192870 MW; D1BE02AF7AB4BFF CRC64;

Query Match 49.6%; Score 56.5; DB 1; Length 1738;
Best Local Similarity 57.1%; Pred. No. 0.69;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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RT "Primary structure of bovine complement activation fragment C4a, the
RT third anaphylatoxin. Purification and complete amino acid sequence.";
RL Biochem. J. 207:253-260(1982).
RN
RP SEQUENCE OF 78-920 FROM N.A.
RC TISSUE=Liver;
RA Groth D.M.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
CC ANAPHYLATOXIN.
CC -FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
CC C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUCOCYTES.
CC -SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
CC AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
CC -MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
CC PROTEIN.
CC -SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
CC -SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC -----
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CC -----
DR EMBL; U16750; AAA52751.1; -
DR EMBL; U16749; AAA52750.1; -
DR PIR; A01265; A01265.
DR HSP; P01031; 1CPA.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001599; Macrogloblna2.
DR InterPro; IPR001134; Netrin_C.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR Complement pathway; Plasma; Glycoprotein; Sulfation;
  Inflammatory response; Thioester bond.
FT NON_TER 1 1
FT NON_CONS 77 78
FT CHAIN 342 343
FT PROPEP 623 629
FT CHAIN 630 920
FT PEPTIDE 1 77
FT DOMAIN 23 57
FT DISULFID 23 49
FT DISULFID 24 56
FT DISULFID 37 57
FT CROSSLINK 191 194
FT MOD_RES 593 593
FT MOD_RES 596 596
FT MOD_RES 598 598
FT CARBOHYD 504 504
FT CARBOHYD 567 567
SQ SEQUENCE 920 AA; 101881 MW; 1425A0BD945F5497 CRC64;

Query Match 48.7%; Score 55.5; DB 1; Length 920;
Best Local Similarity 57.1%; Pred. No. 0.5;
Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

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DB 23 CC0GDTLPMARTCEORAR 43

RESULT 8

CO4\_RAT STANDARD: PRT: 1737 AA.

AC P08649; Q62895; Q6R403;

DT 01-AUG-1998 (Rel. 08, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Complement C4 precursor [Contains: C4a anaphylatoxin].

OS C4

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RA Chen C.-B., Wallis R.;

RT "Substrate recognition by zymogen and activated forms of mannose-binding protein-associated serine proteases.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-266 FROM N.A.

RC STRAIN=Brown Norway;

RA MEDLINE=22131572; PubMed=12136338;

RT Walter L., Hurt P., Hammeibauer H., Sudbrak R., Guenther E.;

RL "Physical mapping of the major histocompatibility complex class II and class III regions of the rat.";

RN Immunogenetics 54:268-275(2002).

RL [3]

RP SEQUENCE OF 1656-1737 FROM N.A., AND INDUCTION.

RC STRAIN=Sprague-Dawley, TISSUE=Hepatic stellate cells;

RX MEDLINE=86399092; PubMed=8805663;

RA Fimmel C.J., Brown K.E., O'Neill R., Kladey R.D.;

RT "Complement C4 protein expression by rat hepatic stellate cells.";

RL J. Immunol. 157:2601-2609(1996).

RN [4]

RP SEQUENCE OF 678-753.

RX MEDLINE=8834568; PubMed=3262196;

RA Cui L.-X., Ferreri K., Hugli T.E.;

RT "Structural characterization of the C4a anaphylatoxin from rat.";

RL Mol. Immunol. 25:663-671(1988).

RN [5]

RP SEQUENCE OF 678-753.

RA Cui L.-X., Ferreri K., Hugli T.E.;

RT "Characterization of rat anaphylatoxins C4a and C5a.";

RL Fed. Proc. 44:991-991(1985).

CC -1- FUNCTION: C4 plays a central role in the activation of the classical pathway of the complement system. It is processed by activated C1 which removes from the alpha chain the C4a anaphylatoxin.

CC -1- FUNCTION: Derived from proteolytic degradation of complement C4, C4a anaphylatoxin is a mediator of local inflammatory processes. It induces the contraction of smooth muscle, increases vascular permeability and causes histamine release from mast cells and basophilic leukocytes.

CC -1- SUBUNIT: This protein is synthesized as a single-chain precursor of nonidentical chains (alpha, beta and gamma) to form a trimer and, prior to secretion, is enzymatically cleaved to form a trimer of nonidentical chains induced in hepatic stellate cells by iron overload and by gamma-interferon.

CC -1- INDUCTION: Induced in hepatic stellate cells by iron overload and by gamma-interferon.

CC MISCELLANEOUS: C4 is a major histocompatibility complex class-III protein.

CC -1- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.

CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.

CC -1- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 1721.

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CC EMBL: AY149995; XAN72415.1; -

CC EMBL: AY091787; XAN14719.1; -

CC EMBL: U42719; XAA91231.1; ALT\_FRAME.

CC PIR: J10036; J10036.

CC HSSP: P01031; IKJS.

DR GO: GO:0005576; C:extracellular; IDA.

DR GO: GO:0003811; F:complement activity; NAS.

DR GO: GO:0006958; P:complement activation, classical pathway; NAS.

DR GO: GO:0006954; P:inflammatory response; NAS.

DR GO: GO:0045987; P:positive regulation of smooth muscle contractility; NAS.

DR InterPro: IPR002890; A2M\_N.

DR InterPro: IPR000020; Anaphylatoxin.

DR InterPro: IPR001840; Anaphylatoxin.

DR InterPro: IPR001599; Macroglobulin2.

DR Pfam: PF01821; Anato\_C.

DR PRINTS: PR00004; ANAPHYLATOXN.

DR ProDom: PD003264; Anaphylatoxin; 1.

DR SMART: SM00104; ANATO; 1.

DR SMART: SM00643; C345C; 1.

DR PROSITE: PS00477; ALPHA\_2\_MACROGLOBULIN; 1.

DR PROSITE: PS01177; ANAPHYLATOXIN\_1; 1.

DR PROSITE: PS01178; ANAPHYLATOXIN\_2; 1.

KW Complement pathway; Glycoprotein; Sulfation; Signal;

KW Inflammatory response; Thioester bond.

FT CHAIN 1

FT SIGNAL 19

FT CHAIN 20

FT PROPEP 674

FT CHAIN 678

FT PROPEP 1443

FT CHAIN 1447

FT PEPTIDE 678

FT DOMAIN 700

FT DOMAIN 1583

FT DISULFID 700

FT DISULFID 701

FT DISULFID 714

FT CROSSLINK 1005

FT MOD\_RES 1412

FT MOD\_RES 1414

FT MOD\_RES 1416

FT MOD\_RES 1676

FT CARBOHYD 224

FT CARBOHYD 664

FT CARBOHYD 743

FT CARBOHYD 1323

FT CARBOHYD 1386

FT CONFLICT 706

FT CONFLICT 1700

FT CONFLICT 1709

FT CONFLICT 1731

SEQUENCE 1737 AA; 192161 MW; 67FA7BFA27A3DDFA CRC64;

Query Match 48.7%; Score 55.5; DB 1; Length 1737;

Best Local Similarity 57.1%; Pred. No. 1;

Matches 12; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYD-ASYNNDTCORAR 20

DB 700 CC0GDTLPMARTCEORAR 720

RESULT 9



CO4\_HUMAN STANDARD; PRT; 1744 AA.  
 ID CO4\_HUMAN  
 AC P01528; Q13160; Q14835; Q5NP65; Q5U1P5;  
 DT 21-UTR-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Complement C4 precursor (Contains: C4A anaphylatoxin).  
 GN C4A AND C4B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A. (C4A AND C4B).  
 RC TISSUE=Liver;  
 RX MEDLINE=84156544; PubMed=6546707;  
 RA Belt K.T., Carroll M.C., Porter R.R.;  
 RT "The structural basis of the multiple forms of human complement  
 component C4.";  
 RL Cell 36:907-914(1984).  
 [2]  
 RP SEQUENCE FROM N.A. (C4A).  
 RX MEDLINE=91108039; PubMed=1988494;  
 RA Yu C.Y.;  
 RT "The complete exon-intron structure of a human complement component  
 C4A gene. DNA sequences, polymorphism, and linkage to the  
 21-hydroxylase gene.";  
 RL J. Immunol. 146:1057-1066(1991).  
 [3]  
 RP SEQUENCE FROM N.A. (C4B).  
 RC TISSUE=Blood;  
 RX MEDLINE=96163032; PubMed=8575831;  
 RA Ulgietti D., Townsend D.C., Christensen F.T., Dawkins R.L.,  
 RA Abraham L.U.;  
 RT "Complete sequence of the complement C4 gene from the HLA-A1, B8,  
 C4A0, C4B1, DR3 haplotype.";  
 RL Immunogenetics 43:250-252(1996).  
 [4]  
 RP SEQUENCE FROM N.A. (C4B).  
 RA Rowen L., Dankers C., Baakin D., Faust J., Loretz C., Ahearn M.E.,  
 RA Santa A., Swartzell S., Smith T.M., Spies T., Hood L.;  
 RT "Sequence determination of 300 kilobases of the human class III MHC  
 locus.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A. (C4A).  
 RA Barlow K.;  
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP SEQUENCE OF 1-22 AND 1056-1225 FROM N.A.  
 RX MEDLINE=85156269; PubMed=3835531;  
 RA Belt K.T., Yu C.Y., Carroll M.C., Porter R.R.;  
 RT "Polymorphism of human complement component C4.";  
 RL Immunogenetics 21:173-180(1985).  
 [7]  
 RP SEQUENCE OF 680-756.  
 RX MEDLINE=81264286; PubMed=6167582;  
 RA Moon K.E., Gorski J.P., Hugli T.E.;  
 RT "Complete primary structure of human C4a anaphylatoxin.";  
 RL J. Biol. Chem. 256:8685-8692(1981).  
 [8]  
 RP SEQUENCE OF 957-1044.  
 RX MEDLINE=82182029; PubMed=6978711;  
 RA Campbell R.D., Gagnon J., Porter R.R.;  
 RT "Amino acid sequence around the thiol and reactive acyl groups of  
 human complement component C4.";  
 RL Biochem. J. 199:359-370(1981).  
 [9]  
 RP SEQUENCE OF 990-1037.  
 RX MEDLINE=82150875; PubMed=6950384;  
 RA Harrison R.A., Thomas M.L., Tack B.F.;  
 RT "Sequence determination of the thiolester site of the fourth  
 component of human complement.";

Proc. Natl. Acad. Sci. U.S.A. 78:7388-7392(1981).  
 [10]  
 RP SEQUENCE OF 1-21 FROM N.A.  
 RX MEDLINE=94282044; PubMed=8012361;  
 RA Sargent C.A., Anderson M.J., Heisler S.L., Kendall E.,  
 RA Gomez-Becobar N., Campbell R.D.;  
 RT "Characterisation of the novel gene G11 lying adjacent to the  
 complement C4A gene in the human major histocompatibility complex.";  
 RL Hum. Mol. Genet. 3:481-488(1994).  
 [11]  
 RP SEQUENCE OF 1405-1431, AND SUFFRATON.  
 RX MEDLINE=86111851; PubMed=3944109;  
 RA Horton G., Sims H., Strauss A.W.;  
 RT "Identification of the site of sulfation of the fourth component of  
 human complement.";  
 RL J. Biol. Chem. 261:1786-1793(1986).  
 [12]  
 RP STRUCTURAL BASIS OF POLYMORPHISM.  
 RX MEDLINE=87080272; PubMed=2431902;  
 RA Yu C.Y., Belt K.T., Giles C.M., Campbell R.D., Porter R.R.;  
 RT "Structural basis of the polymorphism of human complement components  
 C4A and C4B: gene size, reactivity and antigenicity.";  
 RL EMBO J. 5:2873-2881(1986).  
 [13]  
 RP VARIANT C4A6 ALLOTYPES.  
 RX MEDLINE=92242905; PubMed=1573268;  
 RA Anderson M.J., Milner C.M., Cotton G.H., Campbell R.D.;  
 RT "The coding sequence of the hemolytically inactive C4A6 allele of  
 human complement component C4 reveals that a single arginine to  
 tryptophan substitution at beta-chain residue 458 is the likely cause  
 of the defect.";  
 RL J. Immunol. 148:2795-2802(1992).  
 [14]  
 RP FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE  
 CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY  
 ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A  
 ANAPHYLATOXIN.  
 [15]  
 RP FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,  
 C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT  
 INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR  
 PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND  
 BASOPHILIC LEUKOCYTES.  
 [16]  
 RP SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR  
 AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER  
 OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).  
 [17]  
 RP POLYMORPHISM: HUMAN COMPLEMENT COMPONENT C4 IS POLYMORPHIC WITH AT  
 LEAST TWO LOCI, C4A AND C4B. 13 ALLELES OF C4A AND 22 ALLELES OF  
 C4B HAVE BEEN DETECTED. THE ALLELE SHOWN HERE IS C4A4.  
 [18]  
 RP POLYMORPHISM: THE C4A ALLELES CARRY THE BLOOD GROUP RODGERS WHILE  
 THE C4B ALLELES CARRY THE BLOOD GROUP CHIDO.  
 [19]  
 RP DISEASE: Defects in C4A are the cause of C4A deficiency  
 [MIM:120810].  
 [20]  
 RP DISEASE: The C4A6 allele is totally deficient in hemolytic  
 activity.  
 [21]  
 RP MISCELLANEOUS: C4A ALLOTYPES REACT MORE RAPIDLY WITH THE AMINO  
 GROUP OF PEPTIDE ANTIGENS WHILE C4B ALLOTYPES REACT MORE RAPIDLY  
 WITH THE HYDROXYL GROUP OF CARBOHYDRATE ANTIGENS.  
 [22]  
 RP MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III  
 PROTEIN.  
 [23]  
 RP SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.  
 [24]  
 RP SIMILARITY: Contains 1 anaphylatoxin-like domain.  
 [25]  
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 EMBL; K02403; AAB59537.1; -  
 EMBL; K02404; AAB59651.1; -  
 EMBL; M59815; AAB51855.1; -  
 EMBL; M59816; AAB51855.1; JOINED.

```

DR EMBL: U24578; AAA9717.1; -
DR EMBL: AF019413; AAB67980.1; -
DR EMBL: AL049547; CAB89302.1; -
DR EMBL: M14823; AAA55617.1; -
DR EMBL: M14824; AAA52292.1; -
DR EMBL: X77491; CAA54627.1; -
DR PIR: I56095; C4HT.
DR HSSP: P01031; 1K0S.
DR SWISS-2DPAGE; P01028; HUMAN.
DR Genew; HGNC:1323; C4A.
DR MIM; 120810; -.
DR MIM; 120820; -.
DR MIM; 120790; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0006958; P:inflammatory response; NAS.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR GO; GO:0006937; P:regulation of muscle contraction; NAS.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001599; Macroglobulin2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Plasma; Glycoprotein; Sulfation; Signal;
KW Inflammatory response; Polymorphism; Disease mutation;
KW Blood group antigen; Thioester bond.
FT SIGNAL 1
FT CHAIN 20
FT PROPEP 675
FT CHAIN 676
FT PROPEP 679
FT CHAIN 680
FT PROPEP 1446
FT CHAIN 1447
FT CHAIN 1453
FT CHAIN 1454
FT PRETIDE 1744
FT DOMAIN 680
FT DISULFID 702
FT DISULFID 702
FT DISULFID 703
FT DISULFID 735
FT CROSSLNK 1010
FT MOD_RES 1013
FT MOD_RES 1417
FT MOD_RES 1420
FT MOD_RES 1420
FT MOD_RES 1422
FT CARBOHYD 226
FT CARBOHYD 862
FT CARBOHYD 1328
FT CARBOHYD 1391
FT VARIANT 477
Query Match 45.2%; Score 51.5; DB 1; Length 1744;
Best Local Similarity 52.4%; Pred. No. 4.4;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
QY 1 CCYDGA5-VNNDETCEGRAR 20
Db 702 CCQDGVTRLPMMSRCEGRAR 722

```

```

OS Beet necrotic yellow vein mosaic virus (isolate G1).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=12257;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouzoubaa S., Guille H., Jonard G., Richards K., Putz C.;
RT "Nucleotide sequence analysis of RNA-3 and RNA-4 of beet necrotic
RL yellow vein virus, isolates P2 and G1.",
J. Gen. Virol. 66:1553-1564 (1985).
CC -----
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CC -----
DR EMBL: M36897; AAA42800.1; -
DR PIR: C44503; C44503.
DR InterPro; IPR007004; DUF656.
DR Pfam; PF04920; DUF656; 1.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31869 MW; AA7C0351C54FE0CC CRC64;

Query Match 42.1%; Score 48; DB 1; Length 282;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 CCYDGA5VNNDETCE 15
Db 115 CCQDGVLDSELC 128

RESULT 11
OVOS_CHICK
ID OVOS_CHICK STANDARD; PRT; 1473 AA.
AC P20740;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Ovostatin precursor (Ovomacroglobulin).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Gallinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oviduct;
RX MEDLINE=95218210; PubMed=7535598;
RA Nielsen K.L., Sottrup-Jensen L., Nagase H., Thøgersen H.C.,
RA Etzerodt M.;
RT "Amino acid sequence of hen ovomacroglobulin (ovostatin) deduced from
RT cloned cDNA.",
J. Biol. Chem. 258:7481-7489 (1983).
RL DNA Seq. 5:111-119 (1994).
RN [2]
RP SEQUENCE OF 37-49.
RC TISSUE=Egg white;
RX MEDLINE=8328315; PubMed=6408074;
RA Nagase H., Harris E.D., Jr., Woessner J.F., Brew K.;
RT "Ovostatin: a novel proteinase inhibitor from chicken egg white. I.
RT Purification, physicochemical properties, and tissue distribution of
RT ovostatin.",
J. Biol. Chem. 258:7481-7489 (1983).
RN [3]
RP SEQUENCE OF 976-1028.
RC TISSUE=Egg white;
RX MEDLINE=93192299; PubMed=7680577;
RA Nielsen K.L., Sottrup-Jensen L.;
RT "Evidence from sequence analysis that hen egg-white ovomacroglobulin
RT (ovostatin) is devoid of an internal beta-Cys-gamma-Glu thio
RT ester.",

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CC -----
DR EMBL; X98697; CAA67257.1; -.
DR PIR; S65551; S65551.
DR HSSP; P10998; IVD.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; Sushi; 1.
DR SMART; SM0032; CCP; 1.
DR KW Complement alternate pathway; Plasma; Repeat; Sushi.
FT NON_TER 1 1
FT NON_CONS 16 17
FT DOMAIN <17 67 SUSHI 2.
FT DOMAIN 70 131 SUSHI 3.
FT DOMAIN 134 188 SUSHI 4.
FT DOMAIN 191 246 SUSHI 5.
FT DOMAIN 249 309 SUSHI 6.
FT DOMAIN 311 366 SUSHI 7.
FT DOMAIN 370 429 SUSHI 8.
FT DOMAIN 431 488 SUSHI 9.
FT DOMAIN 491 547 SUSHI 10.
FT DOMAIN 553 609 SUSHI 11.
FT DOMAIN 614 668 SUSHI 12.
FT DOMAIN 675 685 SUSHI 13.
FT DISULFID 39 66 BY SIMILARITY.
FT DISULFID 71 117 BY SIMILARITY.
FT DISULFID 103 130 BY SIMILARITY.
FT DISULFID 135 176 BY SIMILARITY.
FT DISULFID 162 187 BY SIMILARITY.
FT DISULFID 192 234 BY SIMILARITY.
FT DISULFID 219 245 BY SIMILARITY.
FT DISULFID 250 297 BY SIMILARITY.
FT DISULFID 280 308 BY SIMILARITY.
FT DISULFID 312 354 BY SIMILARITY.
FT DISULFID 339 365 BY SIMILARITY.
FT DISULFID 371 417 BY SIMILARITY.
FT DISULFID 400 428 BY SIMILARITY.
FT DISULFID 432 476 BY SIMILARITY.
FT DISULFID 459 487 BY SIMILARITY.
FT DISULFID 492 534 BY SIMILARITY.
FT DISULFID 520 546 BY SIMILARITY.
FT DISULFID 554 597 BY SIMILARITY.
FT DISULFID 583 608 BY SIMILARITY.
FT DISULFID 615 656 BY SIMILARITY.
FT DISULFID 642 667 BY SIMILARITY.
FT NON_TER 685 685
SQ SEQUENCE 685 AA; 77536 MW; 69FC9DC8D530E872 CRC64;

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05 Caenorhabditis elegans.
06 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabdioidea;
07 Rhabditidae; Peloderinae; Caenorhabditis.
08 NCBI_TaxID=6239;
09 [1]
10 SEQUENCE FROM N.A.
11 STRAIN=Bristol N2; PubMed=7906398;
12 MEDLINE=94150718;
13 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
14 Bortfield J., Burton J., Connell M., Cosey T., Cooper J., Coulson A.,
15 Craton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
16 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
17 Johnston L., Jones M., Kershaw J., Kirsten J., LaSater N.,
18 Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
19 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
20 Sims M., Smalton N., Smith A., Smith M., Sonhammer B., Staden R.,
21 Sulten J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
22 Waterston J., Watson A., Weinstock L., Wilkinson-Sprat J.,
23 Wohldman P.;
24 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
25 elegans.";
26 Nature 368:32-38(1994).
27 [2]
28 REVISIONS.
29 Waterston R.;
30 Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
31 [3]
32 FUNCTION, AND TISSUE SPECIFICITY.
33 Schaffer M.R., Sanchez B.M., Kenyon C.J.;
34 PubMed=8807295;
35 "Genes affecting sensitivity to serotonin in Caenorhabditis elegans.";
36 Genetics 163:1219-1230(1996).
37 -1- FUNCTION: May act as an auxiliary subunit of the UNC-2 voltage-
38 gated calcium channel which appears to trigger calcium-activated
39 signaling pathways that control the serotonin response. Inhibiting
40 serotonin sensitivity of the vulval muscles results in egg laying
41 defects. May act in both neurons and muscle cells to enhance motor
42 activity.
43 -1- TISSUE SPECIFICITY: Descendants of the cells AB and AB.p (that give
44 rise to nearly all nonpharyngeal neurons), descendants of PL (that
45 give rise to body muscle) and cell lineages that give rise to the
46 adult and juvenile motor neurons.
47 -1- SIMILARITY: Contains 1 WVF domain.
48 -----
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56 -----
57 EMBL; L14433; AAA27971.3; -.
58 PIR; S44617; S44617.
59 WormPep; C50C3.9; C822168.
60 InterPro; IPR004010; Cache.
61 InterPro; IPR002035; WVF_A.
62 Pfam; PR02743; Cache; 1.
63 Pfam; PF00092; WVF; 1.
64 SMART; SM00327; WVF; 1.
65 PROSITE; PS00234; WVF; 1.
66 Behavior; Ionic channel; Ion transport; Voltage-gated channel;
67 Calcium channel; Signal; Glycoprotein.
68 KW SIGNAL 1 19
69 CHAIN 20 1249
70 DOMAIN 250 479 WVF.
71 CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
72 CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
73 CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
74 CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
75 CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
76 CARBOHYD 558 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
77 CARBOHYD 757 757 N-LINKED (GLCNAC. . .) (POTENTIAL).

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OM protein - protein search, using sw model

Run on: December 9, 2003, 14:05:48 ; Search time 21 Seconds

(without alignments)  
91.589 Million cell updates/sec

Title: US-09-651-685A-5  
Perfect score: 114  
Sequence: 1 CCYDASVNNDETCEQPAR 20

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	109	95.6	1676	1	CSHU	complement C5 preect
2	94	82.5	74	2	A25408	complement C5 - bo
3	93	81.6	74	2	A01268	complement C5 - p
4	84	73.7	77	2	A57689	complement C5a - r
5	84	73.7	1680	1	CSMS	complement C5 preec
6	56.5	49.6	1735	2	SS4784	sex-limited protei
7	56.5	49.6	1736	2	A29176	sex-limited protei
8	56.5	49.6	1738	1	A24538	complement C4 prec
9	55.5	48.7	76	2	J10036	complement C4 ana
10	55.5	48.7	77	2	A01265	complement C4 - bo
11	51.5	45.2	1744	1	C4HU	complement C4A pre
12	48	42.1	135	2	D44503	p19 protein - beet
13	48	42.1	282	2	UC5677	RNA4 protein - Bee
14	48	42.1	282	2	C44503	p31 protein - beet
15	47	41.2	834	2	J01965	hypothetical 94k p
16	46	40.4	1473	2	A20872	ovostatin precursor
17	45.5	39.9	1617	2	T28153	complement C4 - Ch
18	45	39.5	159	2	T86760	conserved hypochet
19	45	39.5	161	2	T21013	hypothetical prote
20	44.5	39.0	161	2	S44619	500C3.9 protein -
21	44.5	39.0	281	2	S73895	hypothetical prote
22	44.5	39.0	669	2	S65551	factor H - bovine
23	44	38.6	68	2	AE3441	17k common-antigen
24	44	38.6	2095	2	S29529	genome polyprotein
25	43.5	38.2	241	2	A59262	tetraspan TSPAN-1
26	43.5	38.2	1651	1	C3NU	complement C3 prec
27	43	37.7	198	2	H90111	26S proteasome, be
28	43	37.7	2	2	T18654	hypothetical prote
29	43	37.7	461	2	AH0373	cysteine-tRNA liga

#### ALIGNMENTS

RESULT 1

CSHU  
complement C5 precursor [validated] - human  
N:Contamin: C5a anaphylatoxin; C5b  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 08-Dec-2000  
C/Accession: A40075; A27689; A01267; A01266; S15121  
R:Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.; Wetsel, R.A.  
J. Immunol. 146, 362-368, 1991  
A>Title: Complete cDNA sequence of human complement pro-C5. Evidence of truncated trans  
A/Reference number: A40075; MUID:91079575; PMID:1984448  
A/Accession: A40075  
A/Molecule type: mRNA  
A/Residues: 1-1676 <HAV>  
A/Cross-references: GB:M57129; NID:g179982; PIDN:AAA51925.1; PID:g179983  
R:Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.  
Biochemistry 27, 1474-1482, 1988  
A>Title: Molecular analysis of human complement component C5: localization of the struct  
A/Reference number: A27689; MUID:88209511; PMID:3365401  
A/Accession: A27689  
A/Molecule type: mRNA  
A/Residues: 412-1676 <MET>  
A/Cross-references: GB:M65134; GB:M18879; NID:g179691; PIDN:AAA51856.1; PID:g179692  
R:Fernandez, H.N.; Hugli, T.E.  
J. Biol. Chem. 253, 6955-6964, 1978  
A>Title: Primary structural analysis of the polypeptide portion of human C5a anaphylatox  
A/Reference number: A01267; MUID:79005687; PMID:690134  
A/Accession: A01267  
A/Molecule type: protein  
A/Residues: 678-751 <FER>  
R:Lundvall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead, A.S.; Woods, D.E.; Ogden, R.C.  
J. Biol. Chem. 260, 2108-2112, 1985  
A>Title: Isolation and sequence analysis of a cDNA clone encoding the fifth complement c  
A/Reference number: A01266; MUID:85130937; PMID:2579066  
A/Accession: A01266  
A/Molecule type: mRNA  
A/Residues: 412-854; SLALSPRLCNKGKISGHCKRLPGSSDSASASQVAGITGTHHAQPT' <LUN>  
A/Cross-references: GB:K02874  
R:Bohnack, U.F.; Molitson, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R.  
Biochem. J. 273, 635-640, 1991  
A>Title: Group B streptococci inactivate complement component C5a by enzymic cleavage at  
A/Reference number: S15121; MUID:91144547; PMID:1996961  
A/Accession: S15121  
A/Contents: annotation  
C/Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four  
(beta and alpha chains).  
C/Comment: Activation of C5 initiates the spontaneous assembly of the late complement co  
is the foundation upon which the membrane attack complex is assembled.  
C/Comment: C5a has potent spasmogenic and chemotactic activity.  
C/Genetics:  
A/Genes: GDB:C5

A;Cross-references: GDB:119734; OMIM:120900  
 A;Map position: 9q34.1-9q34.1  
 C;Superfamily: alpha-2-macroglobulin  
 C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I  
 F;1-18/Domain: signal sequence #status predicted <SIG>  
 F;1-673/678-1676/Product: complement C5 #status predicted <SBA>  
 F;1-673/752-1676/Product: C5b #status predicted <CSB>  
 F;1-673/Product: complement C5 and C5b beta chain #status predicted <CSBA>  
 F;678-751/Product: complement C5 alpha chain #status predicted <CSA>  
 F;678-751/Product: C5a anaphylatoxin #status experimental <CSA>  
 F;752-1676/Product: C5b alpha chain #status predicted <CSBA>  
 F;567-810/634-666/698-724/699-731/711-732/866-1527/1101-1159/1375-1505/1405-1474/1520-15  
 F;751/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;751-752/Cleavage site: Arg-Leu (C5 convertase) #status experimental  
 F;911/1115/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.6%; Score 109; DB 1; Length 1676;  
 Best Local Similarity 95.0%; Pred. No. 1.6e-08;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCYDASVNNDETCERAR 20  
 698 CCYDASVNNDETCERAR 717

RESULT 2  
 A25408  
 Complement C5 - bovine (fragment)  
 N;Contains: C5a anaphylatoxin; CSb  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 02-Jun-1988 #sequence\_revision 15-Oct-1994 #text\_change 16-Feb-1997  
 C;Accession: A25408  
 R;Genar: R.; Smonic, T.; Negri, A.; Mottola, C.; Secchi, C.; Ronchi, S.; Romeo, D.  
 Eur. J. Biochem. 155, 77-86, 1986  
 A;Title: C5a fragment of bovine complement. Purification, bioassays, amino-acid sequence  
 A;Reference number: A25408; MUID:8616134; PMID:3081348  
 A;Accession: A25408  
 A;Molecule type: protein  
 A;Residues: 1-74 <GEN>  
 C;Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four  
 (beta and alpha' chains).  
 C;Comment: Activation of C5 initiates the spontaneous assembly of the late complement co  
 is the foundation upon which the membrane attack complex is assembled.  
 C;Comment: C5a has potent spasmogenic and chemotactic activity.  
 C;Superfamily: alpha-2-macroglobulin  
 C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I  
 F;1-74/Product: C5a anaphylatoxin #status experimental <C5T>  
 F;21-47/22-54/34-55/Disulfide bonds: #status predicted

Query Match 82.5%; Score 94; DB 2; Length 74;  
 Best Local Similarity 80.0%; Pred. No. 1.7e-07;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 CCYDASVNNDETCERAR 20  
 21 CCYDASVNNDETCERAR 40

RESULT 3  
 A01268  
 Complement C5 - pig (fragment)  
 N;Contains: C5a anaphylatoxin; CSb  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 29-Jul-1981 #sequence\_revision 15-Oct-1994 #text\_change 16-Feb-1997  
 C;Accession: A01268; A26248  
 R;Genar: C.; Hugli, T.B.  
 J. Biol. Chem. 255, 4710-4715, 1980  
 A;Title: Amino acid sequence of the anaphylatoxin from the fifth component of porcine co  
 A;Reference number: A01268; MUID:8018217; PMID:7372604  
 A;Accession: A01268  
 A;Molecule type: protein  
 A;Residues: 1-74 <GEN>  
 R;Genar: C.; Hugli, T.B.

Proc. Natl. Acad. Sci. U.S.A. 78, 1833-1837, 1981  
 A;Reference number: A26247; MUID:81199549; PMID:6940191  
 A;Contents: annotation; active region  
 A;Note: although Arg-74 is not essential, residues 72-74 (Leu-Gly-Arg) are required for  
 R;Zimmermann, B.; Vogt, W.  
 Hoppe-Seyler's Z. Physiol. Chem. 365, 151-158, 1984  
 A;Reference number: A26248; MUID:84184201; PMID:67114942  
 A;Contents: disulfide bonds  
 A;Accession: A26248  
 A;Molecule type: protein  
 A;Residues: 1-64, 'E', 66-73 <ZIM>  
 C;Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four  
 (beta and alpha' chains).  
 C;Comment: Activation of C5 initiates the spontaneous assembly of the late complement co  
 is the foundation upon which the membrane attack complex is assembled.  
 C;Comment: C5a has potent spasmogenic and chemotactic activity.  
 C;Superfamily: alpha-2-macroglobulin  
 C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I  
 F;1-74/Product: C5a anaphylatoxin #status experimental <C5T>  
 F;21-47/22-54/34-55/Disulfide bonds: #status experimental

Query Match 81.6%; Score 93; DB 2; Length 74;  
 Best Local Similarity 80.0%; Pred. No. 2.4e-07;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 CCYDASVNNDETCERAR 20  
 21 CCYDASVNNDETCERAR 40

RESULT 4  
 A57689  
 Complement C5a - rat (fragment)  
 N;Contains: C5a anaphylatoxin; CSb  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 23-Feb-1996 #sequence\_revision 31-Jan-1997 #text\_change 16-Feb-1997  
 C;Accession: A57689  
 R;Gen: L.; Carney, D.F.; Hugli, T.E.  
 Protein Sci. 3, 1169-1177, 1994  
 A;Title: Primary structure and functional characterization of rat C5a: an anaphylatoxin  
 A;Reference number: A57689; MUID:95078724; PMID:7987212  
 A;Accession: A57689  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-77 <CUI>  
 C;Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four  
 (beta and alpha' chains).  
 C;Function: activation of C5 initiates spontaneous assembly of the late complement co  
 is the foundation for assembly of the membrane attack complex  
 A;Pathway: complement alternate pathway; complement pathway  
 A;Note: C5a has potent spasmogenic and chemotactic activity  
 C;Superfamily: alpha-2-macroglobulin  
 C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I  
 F;1-77/Product: C5a anaphylatoxin #status experimental <C5T>  
 F;24-50/25-57/37-58/Disulfide bonds: #status predicted

Query Match 73.7%; Score 84; DB 2; Length 77;  
 Best Local Similarity 75.0%; Pred. No. 6e-06;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CCYDASVNNDETCERAR 20  
 24 CCYDASVNNDETCERAR 43

RESULT 5  
 C5MS  
 Complement C5 precursor - mouse  
 N;Contains: C5a anaphylatoxin; CSb  
 C;Species: Mus musculus (house mouse)  
 C;Date: 19-Nov-1988 #sequence\_revision 15-Oct-1994 #text\_change 18-Jun-1999  
 C;Accession: A35530; A27538; A40429

R:Wetzel, R.A.; Fleischer, D.T.; Haviland, D.L.  
J. Biol. Chem. 265, 2435-2440, 1990  
A>Title: Deficiency of the murine fifth complement component (C5). A 2-base pair gene deletion.  
A:Reference number: A35530; MUID:90153853; PMID:2303408  
A:Accession: A35530  
A:Molecule type: mRNA  
A:Residues: 1-215; 'L' <MET>  
A:Cross-references: GB:13556; GB:105234; NID:g192302; PIDN:AAA7348.1; PID:g309123  
R:Wetzel, R.A.; Oatza, R.T.; Tack, B.F.  
Biochemistry 26, 737-743, 1987  
A>Title: Primary structure of the fifth component of murine complement.  
A:Reference number: A27538; MUID:87185363; PMID:2436653  
A:Accession: A27538  
A:Molecule type: mRNA  
A:Residues: 'BGL', 44-1580 <MET>  
R:Haviland, D.L.; Haviland, U.C.; Fleischer, D.T.; Wetzel, R.A.  
J. Biol. Chem. 266, 11818-11825, 1991  
A>Title: Structure of the murine fifth complement component (C5) gene. A large, highly polymorphic gene.  
A:Reference number: A40429; MUID:91268053; PMID:1711041  
A:Accession: A40429  
A:Molecule type: DNA  
A:Residues: 1-115 <HVA>  
A:Cross-references: GB:M64952  
C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four amino acids from the C5 protein.  
C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement cascade, the foundation upon which the membrane attack complex is assembled.  
C:Comment: C5a has potent spasmogenic and chemotactic activity.  
C:Genetics:  
A:Map position: 2  
A:Introns: 22/3, 86/3, 140/3, 164/3, 195/2, 223/1, 253/2, 291/3, 334/1, 372/3, 434/3, 504/3, 1224/1, 1292/3, 1343/3, 1364/3, 1392/1, 1411/2, 1445/3, 1470/3, 1506/1, 1534/1, 1564/3  
C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; protein; protein family: alpha-2-macroglobulin  
F:1-18/omains: signal sequence #status predicted <SIG>  
F:19-674/679-1679/Product: complement C5 #status predicted <MAT>  
F:19-674/756-1679/Product: C5b #status predicted <CSB>  
F:19-674/Product: complement C5 and C5b beta chain #status predicted <CSBA>  
F:679-1679/Product: complement C5 alpha chain #status predicted <CSA>  
F:679-756/Product: C5a anaphylatoxin #status predicted <CST>  
F:756-1679/Product: C5b alpha' chain #status predicted <CSBA>  
F:756-814, 635-670, 702-728, 703-725, 715-736, 870-1531, 1105-1163, 1379-1509, 1409-1478, 1524-1531, 1119, 1633/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:915, 1119, 1633/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.7%; Score 84; DB 1; Length 1680;  
Best Local Similarity 75.0%; Pred. No. 0.00011;  
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCYDASVNDTCORAR 20  
Db 702 CCYDARVNYETCERVAR 721

RESULT 6  
S54784  
sex-limited protein Slp(w7) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S54784; 148770  
R:Ogata, R.T.; Zepte, N.E.  
J. Immunol. 147, 2756-2763, 1991  
A>Title: The murine Slp gene. Additional evidence that sex-limited protein has no biological function.  
A:Reference number: S54784; MUID:92013090; PMID:1918990  
A:Accession: S54784  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1135 <OGA>  
A:Cross-references: EMBL:M64933; NID:g200988; PIDN:AAA0117.1; PID:g200989  
R:Hemenway, C.; Kaliff, M.; Stevehagen, J.; Walthall, D.; Robins, D.  
Nucleic Acids Res. 14, 2539-2554, 1986  
A>Title: Sequence comparison of alleles of the fourth component of complement (C4) and sex-limited protein (Slp) genes.  
A:Reference number: 148274; MUID:86176748; PMID:3008092

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A:Accession: I48770
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 634-641, 'L', 643-828 <RES>
A:Cross-references: EMBL:X06455; NID:g54102; PIDD:CAA2961.1; PID:g899336
C:Genetics:
A:Introns: 22/2; 86/3; 154/1; 177/3; 207/2; 235/1; 267/2; 302/3; 347/1; 385/3; 444/3; 50
3; 1219/1; 1296/3; 1352/3; 1372/3; 1404/1; 1464/2; 1494/3; 1519/3; 1554/1; 1584/1; 1617/
3; superfamily: alpha-2-macroglobulin
Query Match 49.6%; Score 56.5; DB 2; Length 1735;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
Cy 1 CCYDG-ASVNNDETCGPAPR 20
Db 700 CCQDSMTKLPKRTCEGPAPR 720
RESULT 7
A29176
sex-limited protein precursor - mouse
N:Alternate names: complement component C4-related sex-limited protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1998 #sequence revision 30-Jun-1998 #ext change 16-Jul-1999
C:Accession: A29176; B21692; A41195; B29059; B60227; I79467
R:Ogata, R.T.; Sepich, D.S.
J. Immunol. 135, 4239-4244, 1985
A>Title: Murine sex-limited protein: complete cDNA sequence and comparison with murine f
A:Reference number: A29176; MUID:86060918; PMID:3840026
A:Accession: A29176
A:Molecule type: mRNA
A:Residues: 1-1736 <OGA>
R:Nonaka, M.; Takahashi, M.; Natsunne-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.; Ho
Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984
A>Title: Isolation of cDNA clones specifying the fourth component of mouse complement an
A:Reference number: A94013; MUID:85038607; PMID:6208559
A:Accession: B21692
A:Molecule type: mRNA
A:Residues: 651-749, 'H', 751-774, 'D', 776-802, 921-1040 <NON>
R:Ogata, R.T.; Sepich, D.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984
A>Title: Genes for murine fourth complement component (C4) and sex-limited protein (Slp)
A:Reference number: A41195; MUID:84272739; PMID:6589636
A:Accession: A41195
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1345-1438, 'R', 1440-1544 <OG2>
A:Cross-references: GB:K02293; NID:g199611; PIDD:AAA39682.1; PID:g199612
R:Toei, M.; Levi-Strauss, M.; Duponchel, C.; Mco, T.
Philos. Trans. R. Soc. Lond. 306, 389-394, 1984
A>Title: Sequence heterogeneity of murine complementary DNA clones related to the C4 and
A:Reference number: A93753
A:Accession: B29059
A:Molecule type: mRNA
A:Residues: 1255-1335, 'G', 1337-1373 <TOS>
R:Ogata, R.T.; Zepf, N.E.
Eur. J. Immunol. 20, 1607-1610, 1990
A>Title: C4 from C4-high and C4-low mouse strains have identical sequences in the region
A:Reference number: A60227; MUID:90353398; PMID:2387317
A:Accession: B60227
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1096-1139 <OG3>
A:Cross-references: GB:X55495
R:Nonaka, M.; Kimura, H.; Yeu, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986
A>Title: Identification of the 5'-flanking regulatory region responsible for the differe
A:Reference number: I59084; MUID:87017050; PMID:3464002
A:Accession: I79467
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>

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A/Cross-references: GB:M14226; NID:g199615; PIDN:AAA39684.1; PID:g554239  
 C/Genetics: slp  
 A/Gene: slp  
 C/Superfamily: alpha-2-macroglobulin  
 F/1-19/Domain: signal sequence #status predicted <SIG>  
 F/20-1736/Product: sex-limited protein #status predicted <MAR>

Query Match 49.6%; Score 56.5; DB 2; Length 1736;  
 Best Local Similarity 57.1%; Pred. No. 2;  
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDG-ASVANDCEGQRAAR 20  
 |||||  
 Db 700 CCODGWTKLPMKRTCEGRAR 720

RESULT 8  
 A24558  
 Complement C4 precursor - mouse  
 N/Contents: classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C4b subunit; cd  
 C/Species: Mus musculus (house mouse)  
 C/Date: 31-Mar-1989 #sequence, revision 11-Nov-1994 #text, change 18-Jun-1999  
 C/Accession: A24558; A25371; A21692; A30520; A60227; A22039; A29059; A01264; B41195; I59  
 R/Sepich, D.S.; Noonan, D.J.; Ogata, R.T.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 5895-5899, 1985  
 A/Title: Complete cDNA sequence of the fourth component of murine complement.  
 A/Reference number: A24558; MUID:85298264; PMID:3862104  
 A/Accession: A24558  
 A/Molecule type: mRNA  
 A/Residues: 1-1738 <SEP>  
 A/Cross-references: GB:M11729; NID:g199080; PIDN:AAA3506.1; PID:g387420  
 A/Experimental source: strain B10.WR  
 R/Nonaka, M.; Nakayama, K.; Yeul, Y.D.; Takahashi, M.  
 U. Biol. Chem. 260, 10936-10943, 1985  
 A/Title: Complete nucleotide and derived amino acid sequences of the fourth component of  
 A/Reference number: A25371; MUID:85289294; PMID:2993295  
 A/Accession: A25371  
 A/Molecule type: mRNA  
 A/Residues: 1133, 'Y', 133-326, 'E', 328-569, 'E', 571-1323, 'N', 1325-1441, 'K', 1443-1452, 'V', 1  
 A/Cross-references: GB:M11789  
 A/Experimental source: strain FM  
 R/Nonaka, M.; Takahashi, M.; Natsumu-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.; Hc  
 Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984  
 A/Title: Isolation of cDNA clones specifying the fourth component of mouse complement an  
 A/Reference number: A94013; MUID:85038607; PMID:6208559  
 A/Accession: A21692  
 A/Molecule type: mRNA  
 A/Residues: 651-719, 'G', 721-738, 'AI', 741-805 <NO2>  
 A/Cross-references: GB:M12970  
 A/Experimental source: strain FM  
 R/Tallon-Miller, P.A.; Sheffler, D.C.  
 U. Immunol. 141, 2362-2387, 1988  
 A/Title: Structural basis for the C4d.1/C4d.2 serologic allotypes of murine complement C  
 A/Reference number: A30520; MUID:89009745; PMID:2459207  
 A/Accession: A30520  
 A/Molecule type: DNA  
 A/Residues: 961-1205, 'Q', 1207-1290 <TAI>  
 A/Cross-references: GB:M23186; NID:g340821; PIDN:AAA40487.1; PID:g554392  
 A/Experimental source: strain B10.BR  
 R/Ogata, R.T.; Zepf, N.E.  
 Eur. J. Immunol. 20, 1607-1610, 1990  
 A/Title: C4 from C4-high and C4-low mouse strains have identical sequences in the region  
 A/Reference number: A60227; MUID:90353398; PMID:2387317  
 A/Accession: A60227  
 A/Molecule type: DNA  
 A/Residues: 1099-1142 <OGA>  
 A/Cross-references: GB:X5593; NID:g287729; PIDN:CAA39112.1; PID:g287730  
 R/Levi-Strauss, M.; Toei, M.; Steimetz, M.; Klein, J.; Meo, T.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 1746-1750, 1985  
 A/Title: Multiple duplications of complement C4 gene correlate with H-2-controlled test  
 A/Reference number: A22039; MUID:85166208; PMID:3856857  
 A/Accession: A22039  
 A/Molecule type: mRNA

A/Residues: 1105-1118, 'A', 1120-1189, 'T', 1191-1449 <LEV>  
 A/Cross-references: GB:K0298; NID:g199281; PIDN:AAQ42021.1; PID:g199282  
 A/Experimental source: strain B10.W7R  
 R/Toei, M.; Levi-Strauss, M.; Duponchel, C.; Meo, T.  
 Philos. Trans. R. Soc. Lond. 306, 389-394, 1984  
 A/Title: Sequence heterogeneity of murine complementary DNA clones related to the C4 and  
 A/Reference number: A93753  
 A/Accession: A29059  
 A/Molecule type: mRNA  
 A/Residues: 1258-1376 <TOS>  
 A/Cross-references: GB:K02798  
 R/Ogata, R.T.; Sheffler, D.C.; Sepich, D.S.; Lilly, S.P.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 5061-5065, 1983  
 A/Title: cDNA clone spanning the alpha-gamma subunit junction in the precursor of the mu  
 A/Reference number: A01264; MUID:83273751; PMID:6192448  
 A/Accession: A01264  
 A/Molecule type: mRNA  
 A/Residues: 1360-1400, 'S', 1402-1511 <OG3>  
 A/Cross-references: GB:K00019; NID:g199259; PIDN:AAA39554.1; PID:g554209  
 A/Experimental source: strain B10.W7R  
 R/Ogata, R.T.; Sepich, D.S.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984  
 A/Title: Genes for murine fourth component (C4) and sex-limited protein (Slp)  
 A/Reference number: A41195; MUID:84272739; PMID:6589636  
 A/Accession: B41195  
 A/Molecule type: mRNA  
 A/Residues: 1360-1400, 'S', 1402-1511 <OG3>  
 A/Cross-references: GB:K00019; NID:g199259; PIDN:AAA39554.1; PID:g554209  
 A/Experimental source: strain B10.W7R  
 R/Nonaka, M.; Kimura, H.; Yeul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986  
 A/Title: Identification of the 5'-flanking regulatory region responsible for the differe  
 A/Reference number: I59084; MUID:87017050; PMID:3464002  
 A/Accession: I59084  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-21 <RES>  
 A/Cross-references: GB:M14225; NID:g199291; PIDN:AAA39563.1; PID:g554211  
 Nucleic Acids Res. 14, 2539-2554, 1986  
 A/Title: Sequence comparison of alleles of the fourth component of complement (C4) and s  
 A/Reference number: I48274; MUID:86176748; PMID:3008092  
 A/Accession: I48274  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 591-603, 'M', 605-1323, 'N', 1325-1452, 'V', 1454-1585, 'Q', 1587-1738 <RE2>  
 A/Cross-references: EMBL:X05314; NID:g50241; PIDN:CAA28936.1; PID:g50242  
 R/Nonaka, M.; Nakayama, K.; Yeul, Y.D.; Shimizu, A.; Takahashi, M.  
 Immunol. Rev. 87, 81-99, 1985  
 A/Title: Molecular cloning and characterization of complementary and genomic DNA clones  
 A/Reference number: I54567; MUID:86031969; PMID:2997024  
 A/Accession: I54567  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-128 <RE3>  
 A/Cross-references: GB:M12968; NID:g199267; PIDN:AAA39558.1; PID:g199270  
 A/Accession: I69023  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1724-1738 <RE4>  
 A/Cross-references: GB:M12969; NID:g199268; PIDN:AAA39559.1; PID:g387439  
 C/Comment: This protein is synthesized as a single-chain precursor and, prior to secreti  
 by disulfide bonds.  
 C/Comment: The activation of complement C4 by complement subcomponent C1s releases the C  
 of complement factor 2 to form the classical-complement-pathway C3 convertase. The C4b,  
 ay C5 convertase.  
 C/Comment: C4a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.  
 C/Comment: The activity of C4b is regulated by proteolytic cleavages involving C4b-bindin  
 C/Genetics: 22/2; 86/3; 97/3; 104/3; 107/3; 1125/3; 1164/3; 1221/3  
 A/Introns: 22/2; 86/3; 97/3; 104/3; 107/3; 1125/3; 1164/3; 1221/3  
 A/Note: The list of introns is incomplete  
 C/Superfamily: alpha-2-macroglobulin  
 C/Keywords: acute phase; complement classical pathway; glycoprotein; hydrolase; inflamma

F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-673/Product: complement C4 beta chain #status predicted <BET>  
F:20-673/754-1440,1448-1738/Product: complement C4b #status predicted <C4b>  
F:678-1440/Product: complement C4 alpha chain #status predicted <ALP>  
F:754-753/Product: C4a anaphylatoxin #status predicted <C4a>  
F:754-843/Region: C4b-binding protein binding  
F:953-1332/Product: C4d fragment #status predicted <C4d>  
F:1448-1738/Product: complement C4 gamma chain #status predicted <GAM>  
F:224/743,1387/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F:753-754/Cleavage site: Arg-Asn (complement subcomponent C1s) #status predicted  
F:1006-1009/Cross-link: thiolester (Cys-gln) #status predicted

Query Match 49.6%; Score 56.5; DB 1; Length 1738;  
Best Local Similarity 57.1%; Pred. No. 2;  
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDG-ASVNDTCGRRAR 20  
DB 700 CCODGNTKLPKRTCEGRAR 720

RESULT 9  
JL0036  
complement C4a anaphylatoxin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 15-Nov-1996  
C:Accession: JL0036  
R:Cut, L.; Ferreri, K.; Hugli, T.E.  
Mol. Immunol. 25, 663-671, 1988  
A:Title: Structural characterization of the C4a anaphylatoxin from rat.  
A:Reference number: JL0036; MUID:8334569; PMID:3262196  
A:Accession: JL0036  
A:Molecule type: protein  
A:Residues: 1-76 <CU>  
C:Superfamily: alpha-2-macroglobulin  
C:Keywords: complement classical pathway; glycoprotein  
F:66/Binding site: carbohydrate (Aen) (covalent) #status experimental

Query Match 48.7%; Score 55.5; DB 2; Length 76;  
Best Local Similarity 57.1%; Pred. No. 0.15;  
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDG-ASVNDTCGRRAR 20  
DB 23 CCODGNTKLPKRTCEGRAR 43

RESULT 10  
A01265  
complement C4 - bovine (fragment)  
N:Contains: C4a anaphylatoxin; classical-complement-pathway C3/C5 convertase (EC 3.4.21.  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 13-Jun-1983 #sequence\_revision 15-Oct-1994 #text\_change 16-Feb-1997  
C:Accession: A01265  
R:Smith, M.A.; Gerrie, L.M.; Dunbar, B.; Fothergill, J.E.  
Biochem. J. 207, 253-260, 1982  
A:Title: Primary structure of bovine complement activation fragment C4a, the third anaphylatoxin  
A:Reference number: A01265; MUID:83126436; PMID:6760852  
A:Accession: A01265  
A:Molecule type: protein  
A:Residues: 1-77 <SMI>  
C:Superfamily: alpha-2-macroglobulin  
C:Keywords: complement pathway; glycoprotein; hydrolase; inflammation; plasma; serine protease  
F:1-77/Product: C4a anaphylatoxin #status experimental <C4t>

Query Match 48.7%; Score 55.5; DB 2; Length 77;  
Best Local Similarity 57.1%; Pred. No. 0.15;  
Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 CCYDGAS-VNNDTCGRRAR 20  
DB 23 CCODGNTKLPKRTCEGRAR 43

## RESULT 11

complement C4a precursor [validated] - human  
N:Contains: classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C4b subunit; cc  
C:Species: Homo sapiens (hmn)  
C>Date: 25-Feb-1985 #sequence\_revision 23-Aug-1996 #text\_change 08-Dec-2000  
C:Accession: I56095; A29177; B29177; A90845; A19311; A92337; S12866; A17265; A32335; A27  
R:Yu, C.Y.  
U. Immunol. 146, 1057-1066, 1991  
A:Title: The complete exon-intron structure of a human complement component C4a gene. DN  
A:Reference number: I56095; MUID:91108039; PMID:1988494  
A:Accession: I56095  
A:Status: preliminary; translated from GB/EMBL/DDBT  
A:Molecule type: DNA  
A:Residues: 1-1744 <RES>  
A:Cross-references: GB:M59815; NID:g179672; PIDN:AAA51855.1; PID:g179674  
R:Belt, K.T.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.  
Immunogenetics 21, 173-180, 1985  
A:Title: Polymorphism of human complement component C4.  
A:Reference number: A29177; MUID:85156269; PMID:3838531  
A:Accession: A29177  
A:Cross-references: GB:M14823  
A:Molecule type: DNA  
A:Residues: 1056-1225 <BE3>  
A:Cross-references: GB:M14824; NID:g179675; PIDN:AAA52292.1; PID:g553210  
R:Belt, K.T.; Carroll, M.C.; Porter, R.R.  
Cell 36, 907-914, 1984  
A:Title: The structural basis of the multiple forms of human complement component C4.  
A:Reference number: A90845; MUID:84156544; PMID:6546707  
A:Accession: A90845  
A:Molecule type: mRNA  
A:Residues: 20-346; 'S', 348-417, 'A', 419-725, 'P', 727-1200, 'S', 1202-1265, 'S', 1287-1418, 1422  
A:Cross-references: GB:K02403  
R:Carroll, M.C.; Porter, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 80, 264-267, 1983  
A:Title: Cloning of a human complement component C4 gene.  
A:Reference number: A19311; MUID:83117835; PMID:6572000  
A:Accession: A19311  
A:Molecule type: mRNA  
A:Residues: 1195-1285, 'S', 1287-1294 <CAR>  
A:Cross-references: GB:V00502; GB:J00080; NID:g30010; PIDN:CAA33760.1; PID:g1335030  
R:Moore, K.E.; Gorski, J.P.; Hugli, T.E.  
J. Biol. Chem. 256, 8685-8692, 1981  
A:Title: Complete primary structure of human C4a anaphylatoxin.  
A:Reference number: A92337; MUID:81264286; PMID:6167582  
A:Accession: A92337  
A:Molecule type: protein  
A:Residues: 680-725, 'PN', 728-756 <MOO>  
R:Hessing, M.; van't Veer, C.; Hackeng, T.M.; Bouma, B.N.; Iwanaga, S.  
FEBS Lett. 271, 131-136, 1990  
A:Title: Importance of the alpha(3) fragment of complement C4 for the binding with C4b-b  
A:Reference number: S12866; MUID:91032049; PMID:1699796  
A:Accession: S12866  
A:Molecule type: protein  
A:Residues: 757, 'X', 759-771; 980-990 <HES>  
R:Campbell, R.D.; Gagnon, J.; Porter, R.R.  
Biochem. J. 199, 359-370, 1981  
A:Title: Amino acid sequence around the thiol and reactive acyl groups of human compleme  
A:Reference number: A17265; MUID:82182029; PMID:6978711  
A:Accession: A17265  
A:Molecule type: protein  
A:Residues: 957-1012, 'E', 1014-1044 <CAM>  
R:Chakravarti, D.N.; Campbell, R.D.; Porter, R.R.  
Mol. Immunol. 24, 1187-1197, 1987  
A:Title: The chemical structure of the C4d fragment of the human complement component C4  
A:Reference number: A32335; MUID:88094444; PMID:3696167  
A:Accession: A32335  
A:Molecule type: protein  
A:Residues: 957-1012, 'E', 1014-1108, 'I', 1110-1175, 'S', 1177-1270, 'V', 1272-1336 <CHA>

A/Note: 1073-Gly, 1120-Leu, 1121-Ser, 1124-Ile, 1125-His, 1207-Ala, 1210-Arg were also  
 R:Chakravarti, D.N.; Campbell, R.D.; Gagnon, J.  
 FEBS Lett. 154, 387-390, 1983  
 A/Title: Amino acid sequence of a polymorphic segment from fragment C4d of human complement  
 A/Reference number: A27600; MWID:83158189; PMID:6832377  
 A/Accession: A27600  
 A/Molecule type: protein  
 A/Residues: 1199-1270, 'V', 1272-1299, 'V', 1301-1304 <CH2>  
 R:Whitehead, A.S.; Goldberger, G.; Woods, D.E.; Markham, A.F.; Colten, H.R.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 5387-5391, 1983  
 A/Title: Use of a cDNA clone for the fourth component of human complement (C4) for analy  
 A/Reference number: 158991; MWID:8329979; PMID:6577433  
 A/Accession: 158991  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1448-1474 <RE2>  
 A/Cross-references: GB:X00830; NID:G187772; PIDN:AAA6229.1; PID:G187773  
 R:Sargent, C.A.; Anderson, M.J.; Hsieh, S.L.; Kendall, E.; Gomez-Becobar, N.; Campbell,  
 Hum. Mol. Genet. 3, 481-488, 1994  
 A/Title: Characterization of the novel gene G11 lying adjacent to the complement C4a gen  
 A/Reference number: 137396; MWID:94282044; PMID:8012361  
 A/Accession: 137399  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-21 <RE3>  
 A/Cross-references: EMBL:X77491; NID:G453410; PIDN:CAA54627.1; PID:G453411  
 C/Comment: This protein is synthesized as a single-chain precursor and, prior to secreti  
 by disulfide bonds.  
 C/Comment: The activation of complement C4 by complement subcomponent C1s releases the C  
 of complement factor 2 to form the classical complement pathway C3 convertase. The C4b,  
 ay C5 convertase.  
 C/Comment: C4a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.  
 C/Comment: The activity of C4b is regulated by proteolytic cleavage involving C4b-binding  
 C/Comment: Residues 1446 or 1449 may be the carboxyl end of the alpha chain.  
 C/Comment: There are at least two genes coding for C4, C4A and C4B. Each gene has many a  
 C/Genetics:  
 A/Gene: GDB:C4A  
 A/Cross-references: GDB:119732; OMIM:120810  
 A/Map position: 6p21.3-6p21.3  
 A/Intons: 22/2; 88/3; 156/1; 179/3; 209/2; 237/1; 269/2; 304/3; 349/1; 387/3; 447/3; 50  
 3; 1226/1; 1303/3; 1359/3; 1379/3; 1411/1; 1473/2; 1503/3; 1528/3; 1563/1; 1593/1; 1626/  
 C/Superfamily: alpha-2-macroglobulin  
 C/Keywords: acute phase; complement classical pathway; glycoprotein; hydrolase; inflamma  
 F,-19/Domain: signal sequence #status predicted <SIG>  
 F,-20-6/5/Product: complement C4 beta chain #status predicted <BET>  
 F,-20-6/5; 157-1446; 1554-1744/Product: C4b #status predicted <C4B>  
 F,-680-1446/Product: complement C4 alpha chain #status predicted <ALP>  
 F,-680-756/Product: C4a anaphylatoxin #status experimental <C4A>  
 F,-757-845/Region: C4b-binding protein binding  
 F,-957-1336/Product: C4d fragment #status experimental <C4D>  
 F,-1454-1744/Product: complement C4 gamma chain #status predicted <GAM>  
 F,-756-157/Cleavage site: Arg-151a (complement subcomponent C1s) #status experimental  
 F,-1010-1013/Cross-link: thiolster (Cys-Gln) #status experimental  
 F,-1328/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match 45.2%; Score 51.5; DB 1; Length 1744;  
 Best Local Similarity 52.4%; Pred. No. 12;  
 Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;  
 Oy 1 CCYDAS-VNNDETCEORAR 20  
 Db 702 CCODGVTRLPMMRSCORAR 722  
 RESULT 12  
 D44503  
 p19 protein - beet necrotic yellow vein mosaic virus (strain G1)  
 C/Species: beet necrotic yellow vein mosaic virus  
 C/Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 08-Apr-1994  
 C/Accession: D44503  
 R:Bouzoubaa, S.; Guillely, H.; Jonard, G.; Richards, K.; Putz, C.  
 J. Gen. Virol. 66, 1553-1564, 1985  
 A/Title: Nucleotide sequence analysis of RNA-3 and RNA-4 of beet necrotic yellow vein vi

A/Reference number: A44503  
 A/Accession: D44503  
 A/Status: preliminary  
 A/Molecule type: genomic RNA  
 A/Residues: 1-135 <BOU>  
 A/Cross-references: GB:M36894  
 C/Genetics:  
 A/Map position: segment 4  
 Query Match 42.1%; Score 48; DB 2; Length 135;  
 Best Local Similarity 57.1%; Pred. No. 3; 6;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Oy 2 CYDASVNNDETCE 15  
 Db 115 CYSQVAVLSDELCE 128  
 RESULT 13  
 JCS677  
 RN4 protein - Beet necrotic yellow vein mosaic virus  
 C/Species: Beet necrotic yellow vein mosaic virus  
 C/Date: 11-Nov-1997 #sequence\_revision 11-Nov-1997 #text\_change 23-Jan-1998  
 C/Accession: JCS677  
 R:Yu, J.L.; Han, C.G.; Yan, L.L.; Li, D.W.; Liu, Y.  
 Acta Microbiol. Sin. 37, 7-14, 1997  
 A/Title: cDNA cloning, sequence analysis and expression of RN4 from beet necrotic yellow  
 A/Reference number: JCS677  
 A/Accession: JCS677  
 A/Molecule type: mRNA  
 A/Residues: 1-282 <YUA>

Query Match 42.1%; Score 48; DB 2; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 7; 3;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Oy 2 CYDASVNNDETCE 15  
 Db 115 CYSQVAVLSDELCE 128  
 RESULT 14  
 C44503  
 p31 protein - beet necrotic yellow vein mosaic virus (strain F2)  
 C/Species: Beet necrotic yellow vein mosaic virus  
 C/Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 08-Apr-1994  
 C/Accession: C44503  
 R:Bouzoubaa, S.; Guillely, H.; Jonard, G.; Richards, K.; Putz, C.  
 J. Gen. Virol. 66, 1553-1564, 1985  
 A/Title: Nucleotide sequence analysis of RNA-3 and RNA-4 of beet necrotic yellow vein vi  
 A/Reference number: A44503  
 A/Accession: C44503  
 A/Status: preliminary  
 A/Molecule type: genomic RNA  
 A/Residues: 1-282 <BOU>  
 A/Cross-references: GB:M36894  
 C/Genetics:  
 A/Map position: segment 4  
 Query Match 42.1%; Score 48; DB 2; Length 282;  
 Best Local Similarity 57.1%; Pred. No. 7; 3;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Oy 2 CYDASVNNDETCE 15  
 Db 115 CYSQVAVLSDELCE 128  
 RESULT 15  
 JQ1965  
 hypothetical 94k protein - rice stripe virus  
 C/Species: rice stripe virus  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Jun-2000

C:Accession: JQ1965  
R:Takahashi, M.; Toriyama, S.; Hamamatsu, C.; Ishihama, A.  
J. Gen. Virol. 74, 769-773, 1993  
A:Title: Nucleotide sequence and possible ambisense coding strategy of rice stripe virus  
A:Reference number: JQ1964; MUID:93224901; PMID:8468589  
A:Accession: JQ1965  
A:Molecule type: genomic RNA  
A:Residues: 1-834 <TRK>  
A:Cross-references: DDBJ:D13176; NID:G53685; PIDN:BA02470.1; PID:G119491  
C:Superfamily: rice stripe virus hypothetical 94K protein

Query Match 41.2%; Score 47; DB 2; Length 834;  
Best Local Similarity 69.2%; Pred. No. 29;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Q: 2 CYDGASVANDETC 14  
||:|||||  
Db 69 CYNRASVNYFETC 81

Search completed: December 9, 2003, 14:08:25  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 14:13:25 ; Search time 23 Seconds  
(without alignments)  
36.792 Million cell updates/sec

Title: US-09-651-685A-5  
114  
Perfect score: 1 CCYDASVNDTCGRAR 20  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 152073

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	30.7	16	1	US-08-137-800-14
2	35	30.7	16	1	US-08-477-383-14
3	35	30.7	16	1	US-08-487-174-14
4	35	30.7	16	1	US-08-480-750-14
5	35	30.7	19	4	US-09-441-502B-31
6	34.5	30.3	18	1	US-08-137-800-32
7	34.5	30.3	18	1	US-08-477-383-32
8	34.5	30.3	18	1	US-08-487-174-32
9	34.5	30.3	18	1	US-08-480-750-32
10	34	29.8	15	3	US-08-975-040-3
11	34	29.8	19	1	US-08-392-646-18
12	34	29.8	19	3	US-08-975-040-2
13	34	29.8	19	3	US-08-975-040-19
14	34	29.8	19	4	US-09-101-927-17
15	34	29.8	19	4	US-09-101-927-19
16	34	29.8	19	4	US-09-441-502B-30
17	32	28.1	9	4	US-09-106-872A-8
18	32	28.1	18	1	US-08-159-340A-32
19	31	27.2	16	1	US-08-574-763-3
20	31	27.2	20	5	PCT-US95-06726-19
21	30	26.3	11	3	US-08-838-413A-14
22	29.5	25.9	18	1	US-08-137-800-13
23	29.5	25.9	18	1	US-08-137-800-31
24	29.5	25.9	18	1	US-08-477-383-13
25	29.5	25.9	18	1	US-08-477-383-31
26	29.5	25.9	18	1	US-08-487-174-13
27	29.5	25.9	18	1	US-08-487-174-31

#### ALIGNMENTS

28	29.5	25.9	18	1	US-08-480-750-13	Sequence 13, Appl
29	29.5	25.9	18	1	US-08-480-750-31	Sequence 31, Appl
30	29	25.4	10	1	US-08-421-702A-79	Sequence 79, Appl
31	29	25.4	10	1	US-08-303-052A-32	Sequence 32, Appl
32	29	25.4	10	1	US-08-421-696A-79	Sequence 79, Appl
33	29	25.4	10	1	US-08-421-697A-79	Sequence 79, Appl
34	29	25.4	10	1	US-08-421-698A-79	Sequence 79, Appl
35	29	25.4	10	2	US-08-421-695A-32	Sequence 32, Appl
36	29	25.4	10	3	US-08-461-384B-9	Sequence 9, Appl
37	29	25.4	10	3	US-08-407-207A-6	Sequence 6, Appl
38	29	25.4	13	4	US-09-136-769A-7	Sequence 7, Appl
39	29	25.4	13	4	US-09-136-769A-18	Sequence 18, Appl
40	29	25.4	13	4	US-08-335-303-20	Sequence 20, Appl
41	29	25.4	19	1	US-08-290-448A-49	Sequence 49, Appl
42	29	25.4	19	1	US-08-290-448A-49	Sequence 49, Appl
43	29	25.4	19	1	US-08-175-069A-49	Sequence 49, Appl
44	29	25.4	19	1	US-08-175-069A-49	Sequence 49, Appl
45	29	25.4	19	4	US-08-461-939B-49	Sequence 49, Appl

RESULT 1  
US-08-137-800-14  
Sequence 14, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:  
APPLICANT: Oliveira, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Amurfin D.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,800  
FILING DATE: 19-OCT-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-104763  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEO ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6..14  
OTHER INFORMATION: /note="Xaa(6) is Pro or  
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro;  
OTHER INFORMATION: Xaa(14) is Asp or Beta-carboxyaspartate"

US-08-137-800-14

Query Match 30.7%; Score 35; DB 1; Length 16;

Best Local Similarity 42.9%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14  
| : |||||  
Db 3 CSHXACSVNXXIC 16RESULT 2  
US-08-477-383-14

; Sequence 14, Application US/08477383

; Patent No. 5589340

; GENERAL INFORMATION:

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Hillyard, David R.

; APPLICANT: Macintosh, J. Michael

; APPLICANT: Santos, Ameurino S.

; TITLE OF INVENTION: Conotoxin Peptides

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard &amp; Civiletti

; STREET: 1201 New York Avenue, N.W., Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,383

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/137,800

; FILING DATE: 19-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/084,848

; FILING DATE: 29-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24260-107673

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Conus bandanus

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 6..14

; OTHER INFORMATION: /note= "Xaa(6) is Pro or

; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or

; OTHER INFORMATION: beta-carboxyasparsate."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 16

; OTHER INFORMATION: /note= "The C-terminus is

; OTHER INFORMATION: preferably amidated."

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US-08-477-383-14

Query Match 30.7%; Score 35; DB 1; Length 16;

Best Local Similarity 42.9%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14  
| : |||||  
Db 3 CSHXACSVNXXIC 16RESULT 3  
US-08-487-174-14

; Sequence 14, Application US/08487174

; Patent No. 5595972

; GENERAL INFORMATION:

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Hillyard, David R.

; APPLICANT: Macintosh, J. Michael

; APPLICANT: Santos, Ameurino S.

; TITLE OF INVENTION: Conotoxin Peptides

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard &amp; Civiletti

; STREET: 1201 New York Avenue, N.W., Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,174

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/137,800

; FILING DATE: 19-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/084,848

; FILING DATE: 29-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24260-107673

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Conus bandanus

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 6..14

; OTHER INFORMATION: /note= "Xaa(6) is Pro or

; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or

; OTHER INFORMATION: beta-carboxyasparsate."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 16

; OTHER INFORMATION: /note= "The C-terminus is

; OTHER INFORMATION: preferably amidated."

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US-08-487-174-14

Query Match 30.7%; Score 35; DB 1; Length 16;  
Best Local Similarity 42.9%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14  
DB 3 CSHXACSVNXXIC 16

## RESULT 4

US-08-480-750-14  
Sequence 14, Application US/08480750  
Patent No. 5633347  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfin S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6..14  
OTHER INFORMATION: /note="Xaa(6) is Pro or  
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16  
OTHER INFORMATION: /note="The C-terminus is  
OTHER INFORMATION: preferably amidated."

US-08-480-750-14

Query Match 30.7%; Score 35; DB 1; Length 16;  
Best Local Similarity 42.9%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14  
DB 3 CSHXACSVNXXIC 16

## RESULT 5

US-09-441-502B-31  
Sequence 31, Application US/09441502B  
Patent No. 6455041  
GENERAL INFORMATION:  
APPLICANT: Dunbar, Bonita S.  
TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN  
FILE REFERENCE: 1231.2USU1  
CURRENT APPLICATION NUMBER: US/09/441,502B  
CURRENT FILING DATE: 1999-11-17  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 31  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-441-502B-31

Query Match 30.7%; Score 35; DB 4; Length 19;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCYDASVNN 10  
DB 5 CCYSSEVNS 14

## RESULT 6

US-08-137-800-32  
Sequence 32, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfin S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,800  
FILING DATE: 19-OCT-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-104763  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3..4  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"  
US-08-137-800-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;  
Best Local Similarity 46.7%; Pred. No. 45;  
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CCYDGA-SYNDCTC 14  
Db 4 CCSNPACVNNPQIC 18

RESULT 7  
US-08-477-383-32  
Sequence 32, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Aurelio S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus

ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 18  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
US-08-477-383-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;  
Best Local Similarity 46.7%; Pred. No. 45;  
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
QY 1 CCYDGA-SYNDCTC 14  
Db 4 CCSNPACVNNPQIC 18

RESULT 8  
US-08-487-174-32  
Sequence 32, Application US/08487174  
Patent No. 5595972  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Aurelio S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,174  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus



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;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 18
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."
;
US-08-487-174-32

Query Match      30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      1 CCYDGA-SVNNDET 14
Db      4 CCSPACVNNPQIC 18

RESULT 9
US-08-480-750-32
; Sequence 32, Application US/08480750
; Patent No. 5633347
;
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cituz, Lourdes J.
; APPLICANT: Hilliard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Amerfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,750
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION/DOCKET NUMBER: 28,957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus ermineus
; FEATURE:
; NAME/KEY: Modified-site
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;
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 18
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."
;
US-08-480-750-32

Query Match      30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      1 CCYDGA-SVNNDET 14
Db      4 CCSPACVNNPQIC 18

RESULT 10
US-08-975-040-3
; Sequence 3, Application US/08975040
; Patent No. 6251620
;
; GENERAL INFORMATION:
; APPLICANT: HATADA, MARCOS
; APPLICANT: LU, XIADDE
; APPLICANT: LAIRD, ELLEN
; APPLICANT: KARAS, JENNIFER
; APPLICANT: ZOLLER, MARK
; APPLICANT: HOOT, DENNIS
; TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
; TITLE OF INVENTION: TO ZAP-FAMILY PROTEINS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
; INC.
; STREET: 26 LANDSDOWNE STREET
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: US
; ZIP: 02139
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,040
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,578
; FILING DATE: 22-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BERSTEIN, DAVID L.
; REGISTRATION/DOCKET NUMBER: 31,235
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-494-0400
; TELEFAX: 617-494-1828
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "phosphotyrosine"
; OTHER INFORMATION: /label= pTyr
; OTHER INFORMATION: /note= "phosphorylated tyrosine"
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NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /product= "phosphotyrosine"  
OTHER INFORMATION: /label= ptyr  
OTHER INFORMATION: /note= "phosphorylated tyrosine"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "Acetylated"  
OTHER INFORMATION: /label= Ac  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: /product= "amidated"  
OTHER INFORMATION: /label= NH2  
US-08-975-040-3

Query Match 29.8%; Score 34; DB 3; Length 15;  
Best Local Similarity 53.8%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDTCR 15  
DB 1 YTGSLSTRNGETY 13

RESULT 11  
US-08-392-646-18  
Sequence 18, Application US/08392646  
Patent No. 5710129  
GENERAL INFORMATION:  
APPLICANT: LYNCH, Berkley A.  
APPLICANT: WEIGEL, Manfred  
TITLE OF INVENTION: NEW INHIBITORS OF SH2-MEDIATED PROCESSES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landedowne Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139-4234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,646  
FILING DATE: 23-FEB-1995  
CLASSIFICATION: 560  
ATTORNEY/AGENT INFORMATION:  
NAME: BERSTEIN, David L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: ARIAD 337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-0208  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "phosphotyrosine"  
OTHER INFORMATION: /label= YPO4  
OTHER INFORMATION: /note= "phosphorylated tyrosine"  
FEATURE:  
LOCATION: 15

NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: /product= "phosphotyrosine"  
OTHER INFORMATION: /label= YPO4  
OTHER INFORMATION: /note= "phosphorylated tyrosine"  
US-08-392-646-18

Query Match 29.8%; Score 34; DB 1; Length 19;  
Best Local Similarity 53.8%; Pred. No. 56;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDTCR 15  
DB 4 YTGSLSTRNGETY 16

RESULT 12  
US-08-975-040-2  
Sequence 2, Application US/08975040  
Patent No. 6251620  
GENERAL INFORMATION:  
APPLICANT: HATADA, MARCOS  
APPLICANT: LU, XIAODE  
APPLICANT: LAIRD, ELLEN  
APPLICANT: KARAS, JENNIFER  
APPLICANT: ZOLLER, MARK  
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING  
TITLE OF INVENTION: TO ZAP-FAMILY PROTEINS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,  
INC.  
STREET: 26 LANSDOWNE STREET  
CITY: CAMBRIDGE  
STATE: MA  
COUNTRY: US  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,040  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,578  
FILING DATE: 22-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BERSTEIN, DAVID L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: ARIAD 347F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-1828  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "phosphotyrosine"  
OTHER INFORMATION: /label= ptyr  
OTHER INFORMATION: /note= "phosphorylated tyrosine"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15

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; OTHER INFORMATION: /product= "phosphotyrosine"
; OTHER INFORMATION: /label= ptyr
; OTHER INFORMATION: /note= "phosphorylated tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "Acetylated"
; OTHER INFORMATION: /label= Ac
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /product= "amidated"
; OTHER INFORMATION: /label= NH2
; US-08-975-040-2

Query Match      29.8%; Score 34; DB 3; Length 19;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3 YDGASVNDNDETC 15
DB      4 YTGISTRNQETVE 16

RESULT 13
US-08-975-040-19
; Sequence 19, Application US/08975040
; Patent No. 6251620
; GENERAL INFORMATION:
; APPLICANT: HATADA, MARCOS
; APPLICANT: LU, XIADDE
; APPLICANT: LAIRD, ELLEN
; APPLICANT: KARAS, JENNIFER
; APPLICANT: ZOLLER, MARK
; APPLICANT: HOLT, DENNIS
; TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
; TITLE OF INVENTION: TO ZAP-FAMILY PROTEINS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
; ADDRESSEE: INC.
; STREET: 26 LANDSDOWNE STREET
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: US
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975, 040
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/605, 578
; FILING DATE: 22-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BERSTEIN, DAVID L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: ARIAD 347F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-494-0400
; TELEFAX: 617-494-1828
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "phosphotyrosine"
; OTHER INFORMATION: /label= YPO4
; OTHER INFORMATION: /note= "phosphorylated tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /product= "phosphotyrosine"
; OTHER INFORMATION: /label= YPO4
; OTHER INFORMATION: /note= "phosphorylated tyrosine"
; US-08-975-040-19

Query Match      29.8%; Score 34; DB 3; Length 19;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3 YDGASVNDNDETC 15
DB      4 YTGISTRNQETVE 16

RESULT 14
US-09-101-927-17
; Sequence 17, Application US/09101927
; Patent No. 6303319
; GENERAL INFORMATION:
; APPLICANT: Rickles, Richard J
; TITLE OF INVENTION: Cell-Based Assay
; FILE REFERENCE: 336A PCT/US
; CURRENT APPLICATION NUMBER: US/09/101,927
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US97/026735
; EARLIER FILING DATE: 1997-02-21
; EARLIER APPLICATION NUMBER: 60/012,218
; EARLIER FILING DATE: 1996-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (4)_
; OTHER INFORMATION: PHOSPHORYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: PHOSPHORYLATION
; US-09-101-927-17

Query Match      29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3 YDGASVNDNDETC 15
DB      4 YTGISTRNQETVE 16

RESULT 15
US-09-101-927-19
; Sequence 19, Application US/09101927
; Patent No. 6303319
; GENERAL INFORMATION:
; APPLICANT: Rickles, Richard J
; TITLE OF INVENTION: Cell-Based Assay
; FILE REFERENCE: 336A PCT/US
; CURRENT APPLICATION NUMBER: US/09/101,927
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US97/026735
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; EARLIER FILING DATE: 1997-02-21  
; EARLIER APPLICATION NUMBER: 60/012,218  
; EARLIER FILING DATE: 1996-02-23  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)\_RES  
; OTHER INFORMATION: PHOSPHORYLATION  
US-09-101-927-19

Query Match 29.8%; Score 34; DB 4; Length 19;  
Best Local Similarity 53.8%; Pred. No. 56;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 YDGASVNNDETCE 15  
| | | | | | | | | |  
Db 4 YTGSLSTRNQETYE 16

Search completed: December 9, 2003, 14:16:30  
Job time : 24 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 9, 2003, 14:15:25 ; Search time 30 Seconds  
(without alignments)  
123.989 Million cell updates/sec

Title: US-09-651-685a-5

Perfect score: 114  
Sequence: 1 CCYDASVNNDETCEGRAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 145776

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	114	100.0	20	10	US-09-878-603-5
2	111	97.4	20	10	US-09-878-603-68
3	110	96.5	20	10	US-09-878-603-67
4	110	96.5	20	10	US-09-878-603-69
5	110	96.5	20	10	US-09-878-603-70
6	110	96.5	20	10	US-09-878-603-71
7	110	96.5	20	10	US-09-878-603-73
8	109	95.6	19	10	US-09-878-603-54
9	108	94.7	20	10	US-09-878-603-64
10	108	94.7	20	10	US-09-878-603-65
11	106	93.0	20	10	US-09-878-603-72
12	105	92.1	18	10	US-09-878-603-55
13	105	92.1	19	10	US-09-878-603-59
14	102	89.5	20	10	US-09-878-603-66
15	101	88.6	17	10	US-09-878-603-56

16	98	86.0	20	10	US-09-878-603-74	Sequence 74, Appl
17	96	84.2	16	10	US-09-878-603-57	Sequence 57, Appl
18	96	84.2	18	10	US-09-878-603-60	Sequence 58, Appl
19	91	79.8	15	10	US-09-878-603-58	Sequence 60, Appl
20	89	78.1	17	10	US-09-878-603-61	Sequence 61, Appl
21	83	72.8	16	10	US-09-878-603-62	Sequence 62, Appl
22	77	67.5	15	10	US-09-878-603-63	Sequence 63, Appl
23	51	44.7	20	10	US-09-878-603-2	Sequence 2, Appl
24	36	31.6	15	12	US-10-256-277-46	Sequence 46, Appl
25	36	31.6	15	12	US-10-256-277-46	Sequence 46, Appl
26	35.5	31.1	19	15	US-10-072-602B-407	Sequence 407, App
27	35	30.7	16	15	US-10-072-602B-444	Sequence 444, App
28	34.5	30.3	19	15	US-10-072-602B-404	Sequence 404, App
29	34	29.8	18	15	US-10-142-238A-3	Sequence 3, Appl
30	34	29.8	20	10	US-09-321-801-5	Sequence 5, Appl
31	33	28.9	16	15	US-10-072-602B-617	Sequence 617, App
32	33	28.9	17	15	US-10-072-602B-403	Sequence 403, App
33	33	28.9	17	15	US-10-072-602B-404	Sequence 404, App
34	33	28.9	17	15	US-10-072-602B-602	Sequence 602, App
35	33	28.9	17	15	US-10-072-602B-603	Sequence 603, App
36	32	28.1	6	10	US-09-878-603-15	Sequence 15, Appl
37	31	27.2	17	15	US-10-072-602B-606	Sequence 606, App
38	31	27.2	20	12	US-10-159-339-91	Sequence 91, Appl
39	30.5	26.8	16	12	US-10-084-994-16	Sequence 16, Appl
40	30.5	26.8	16	15	US-10-256-277-44	Sequence 44, Appl
41	30	26.3	12	15	US-10-256-277-44	Sequence 44, Appl
42	30	26.3	12	15	US-10-256-277-44	Sequence 44, Appl
43	30	26.3	18	12	US-10-256-277-48	Sequence 48, Appl
44	30	26.3	18	15	US-10-209-323-48	Sequence 48, Appl
45	29	25.4	9	10	US-09-252-150-78	Sequence 78, Appl

## ALIGNMENTS

RESULT 1  
US-09-878-603-5  
; Sequence 5, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarna, Vitya  
; APPLICANT: Czemak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: US-03783  
; CURRENT APPLICATION NUMBER: US/09/878, 603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387, 671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-878-603-5

Query Match 100.0%; Score 114; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 1 CCYDASVNNDETCEGRAR 20  
DB 1 CCYDASVNNDETCEGRAR 20

RESULT 2  
US-09-878-603-68  
; Sequence 68, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.

```

; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 68
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-68

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Query Match          97.4%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CCYDGATVNNDETCEQRAAR 20

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RESULT 3
US-09-878-603-67
; Sequence 67, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 67
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-67

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Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CCYDGASVNNDETCEQRAAR 20

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RESULT 4
US-09-878-603-69
; Sequence 69, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783

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; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-69

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Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 CCYDGVSVNNDETCEQRAAR 20

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RESULT 5
US-09-878-603-70
; Sequence 70, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-70

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Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 CCYDGASVNNDETCEQRAAR 20

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RESULT 6
US-09-878-603-71
; Sequence 71, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74

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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-71
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Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CCYDGASVNNDETCEQRAAR 20
Db      1 CCYDGASVNNDETCEQRAAR 20
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RESULT 7
US-09-878-603-73
; Sequence 73, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-73
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Query Match          96.5%; Score 110; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      1 CCYDGASVNNDETCEQRAAR 20
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RESULT 8
US-09-878-603-54
; Sequence 54, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-54
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Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 CCYDGASVNNDETCEQRAA 19
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RESULT 9
US-09-878-603-64
; Sequence 64, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-64
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Query Match          94.7%; Score 108; DB 10; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      1 CCYDGASVNNDETCEQRAAR 20
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RESULT 10
US-09-878-603-65
; Sequence 65, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 65
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65
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Query Match          94.7%; Score 108; DB 10; Length 20;
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Best Local Similarity 95.0%; Pred. No. 8.4e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 11  
US-09-878-603-72  
; Sequence 72, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czernak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-72

Query Match 93.0%; Score 106; DB 10; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e-09;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 12  
US-09-878-603-55  
; Sequence 55, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czernak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-55

Query Match 92.1%; Score 105; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 18  
Db 1 CCYDASVNNDETCEQRAAR 18

Db 1 CCYDASVNNDETCEQRAAR 18

RESULT 13  
US-09-878-603-59  
; Sequence 59, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czernak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-59

Query Match 92.1%; Score 105; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 19

RESULT 14  
US-09-878-603-66  
; Sequence 66, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czernak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 66  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-66

Query Match 89.5%; Score 102; DB 10; Length 20;  
Best Local Similarity 90.0%; Pred. No. 6.9e-09;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20  
Db 1 CCYDASVNNDETCEQRAAR 20

RESULT 15  
US-09-878-603-56



; Sequence 56, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czermak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-878-603-56

Query Match 88.6%; Score 101; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCYDGASVNNDETCEQR 17  
Db 1 CCYDGASVNNDETCEQR 17

Search completed: December 9, 2003, 14:20:39  
Job time : 30 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 9, 2003, 14:08:29 ; Search time 41 Seconds  
(without alignments)  
77.428 Million cell updates/sec

Title: US-09-651-685A-5  
114  
Sequence: 1 CCYDGASVNDTECEGRAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 400068

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	22	AA874055
2	111	97.4	20	22	AA874111
3	110	96.5	20	22	AA874110
4	110	96.5	20	22	AA874112
5	110	96.5	20	22	AA874113
6	110	96.5	20	22	AA874114
7	110	96.5	20	22	AA874116
8	109	95.6	19	22	AA874097
9	109	95.6	20	22	AA874120

10	108	94.7	20	22	AA874107	C-terminal truncat
11	108	94.7	20	22	AA874108	C-terminal truncat
12	106	93.0	20	22	AA874115	C-terminal truncat
13	105	92.1	18	22	AA874098	C-terminal truncat
14	105	92.1	19	22	AA874102	C-terminal truncat
15	102	89.5	20	22	AA874109	C-terminal truncat
16	101	88.6	17	22	AA874099	C-terminal truncat
17	98	86.0	20	22	AA874117	C-terminal truncat
18	96	84.2	16	22	AA874100	C-terminal truncat
19	96	84.2	18	22	AA874103	C-terminal truncat
20	91	79.8	15	22	AA874101	C-terminal truncat
21	89	78.1	17	22	AA874104	C-terminal truncat
22	83	72.8	16	22	AA874105	C-terminal truncat
23	77	67.5	15	22	AA874106	C-terminal truncat
24	65	57.0	12	24	AA874052	Binding epitope of
25	51	44.7	20	22	AA874052	Rat C5a peptide fr
26	47	41.2	12	24	AA874052	Binding epitope of
27	40.5	35.5	18	21	AA874136	Cone snail alpha-c
28	38.5	33.8	16	21	AA874133	Cone snail alpha-c
29	38.5	33.8	20	21	AA874148	Cone snail alpha-c
30	38	33.3	16	21	AA875274	A-lineage conotoxin
31	38	33.3	16	21	AA875272	Cone snail alpha-c
32	36	31.6	15	23	AA875292	Positive cell sele
33	35.5	31.1	17	21	AA875292	Cone snail alpha-c
34	35.5	31.1	19	23	ABG99638	Conus sp conotoxin
35	35	30.7	16	18	AAW24861	Predatory cone sna
36	35	30.7	16	18	AAW12736	A-lineage conotoxin
37	35	30.7	16	23	ABG99663	Conus sp conotoxin
38	35	30.7	19	24	ABU13434	Zona pellucida pro
39	34.5	30.3	18	16	AAW75292	A-lineage conotoxi
40	34.5	30.3	18	18	AAW24867	Predatory cone sna
41	34.5	30.3	18	18	AAW12751	A-lineage conotoxi
42	34.5	30.3	19	23	ABG99819	Conus sp conotoxin
43	34	29.8	15	18	AAW30137	Tandem SH2 ligand
44	34	29.8	19	15	AAW56639	Tyrosine activatio
45	34	29.8	19	15	AAW56633	Tyrosine activatio

## ALIGNMENTS

## RESULT 1

ID AAB74055 standard; Peptide; 20 AA.

XX AAB74055;

XX 16-MAY-2001 (first entry)

DE Human C5a peptide fragment #2.

XX Human; C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Homo sapiens.

PN WO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

PA (UNMI ) UNIV MICHIGAN.

PI Ward PA, Huber-Iang M, Sarma V;

DR WPI; 2001-226665/23.

XX N-PSDB; AAF75793.  
PT Compositions for treating blood-borne and toxin mediated diseases and

PT treatment of sepsis in humans and other animals comprises anti-C5a  
PT antibodies generated against C-terminal truncated C5a peptides -  
XX  
PS Claim 8, Page 26, 84pp; English.  
XX  
CC The present sequence is a peptide fragment of human complement component  
CC C5a (the full-length sequence is given in AAB74053). The present  
CC invention relates to an antibody specific for the present sequence. The  
CC C5a-antibody can be used in a therapeutic composition, which is useful  
CC for treating a subject suffering from bacterial infection, e.g.  
CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract  
CC infections or infections in wounds. In addition, the C5a antibody can  
CC be used for treating sepsis. C5a is also known as anaphylatoxin.  
XX  
SQ Sequence 20 AA;  
Query Match 100.0%; Score 114; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5,4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CCYDGSVNNDETCEQRAAR 20  
DB 1 CCYDGSVNNDETCEQRAAR 20  
RESULT 2  
AAB74111  
ID AAB74111 standard; Peptide; 20 AA.  
XX  
AC AAB74111;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE C-terminal truncated C5a peptide #49.  
XX  
DE C5a; complement; antibody; bacterial infection; sinusitis;  
XX meningitis; respiratory; gastrointestinal; urinary tract infection;  
XX wound; anaphylatoxin; sepsis.  
XX  
OS Unidentified.  
XX  
PN WO200115731-A1.  
XX  
PD 08-MAR-2001.  
XX  
PF 31-AUG-2000; 2000WO-US24219.  
XX  
PR 31-AUG-1999; 99US-0387671.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Ward PA, Huber-Lang M, Sarma V;  
XX  
DR WPI; 2001-226665/23.  
XX  
PT Compositions for treating blood-borne and toxin mediated diseases and  
PT treatment of sepsis in humans and other animals comprises anti-C5a  
PT antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Page 30; 84pp; English.  
XX  
CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
CC present invention relates to an antibody specific for the present  
CC sequence. The C5a-antibody can be used in a therapeutic composition,  
CC which is useful for treating a subject suffering from bacterial  
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
CC urinary tract infections or infections in wounds. In addition, the C5a  
CC antibody can be used for treating sepsis. C5a is also known as  
CC anaphylatoxin.  
XX  
SQ Sequence 20 AA;  
Query Match 97.4%; Score 111; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 1.6e-10;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CCYDGSVNNDETCEQRAAR 20  
DB 1 CCYDGSVNNDETCEQRAAR 20  
RESULT 3  
AAB74110  
ID AAB74110 standard; Peptide; 20 AA.  
XX  
AC AAB74110;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE C-terminal truncated C5a peptide #48.  
XX  
DE C5a; complement; antibody; bacterial infection; sinusitis;  
XX meningitis; respiratory; gastrointestinal; urinary tract infection;  
XX wound; anaphylatoxin; sepsis.  
XX  
OS Unidentified.  
XX  
PN WO200115731-A1.  
XX  
PD 08-MAR-2001.  
XX  
PF 31-AUG-2000; 2000WO-US24219.  
XX  
PR 31-AUG-1999; 99US-0387671.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Ward PA, Huber-Lang M, Sarma V;  
XX  
DR WPI; 2001-226665/23.  
XX  
PT Compositions for treating blood-borne and toxin mediated diseases and  
PT treatment of sepsis in humans and other animals comprises anti-C5a  
PT antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Page 30; 84pp; English.  
XX  
CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
CC present invention relates to an antibody specific for the present  
CC sequence. The C5a-antibody can be used in a therapeutic composition,  
CC which is useful for treating a subject suffering from bacterial  
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
CC urinary tract infections or infections in wounds. In addition, the C5a  
CC antibody can be used for treating sepsis. C5a is also known as  
CC anaphylatoxin.  
XX  
SQ Sequence 20 AA;  
Query Match 96.5%; Score 110; DB 22; Length 20;  
Best Local Similarity 95.0%; Pred. No. 2,3e-10;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CCYDGSVNNDETCEQRAAR 20  
DB 1 CCYDGSVNNDETCEQRAAR 20  
RESULT 4  
AAB74112  
ID AAB74112 standard; Peptide; 20 AA.  
XX  
AC AAB74112;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE C-terminal truncated C5a peptide #50.

XX C5a; complement; antibody; bacterial infection; sinusitis;  
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KM wound; anaphylatoxin; sepsis.  
 XX Unidentified.  
 OS  
 XX WO200115731-A1.  
 PN  
 XX 08-MAR-2001.  
 PD  
 XX 31-AUG-2000; 2000WO-US24219.  
 PF  
 XX 31-AUG-1999; 99US-0387671.  
 PR  
 XX (UNMI ) UNIV MICHIGAN.  
 PA  
 XX Ward PA, Huber-Lang M, Sarma V;  
 PI  
 XX WPI; 2001-226665/23.  
 DR  
 XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.  
 CC  
 SQ Sequence 20 AA;  
 QY  
 DB 1 CCYDGASVNNDETCEQRRAR 20  
 1 CCYDGASVNNDETCEQRRAR 20  
 DB 1 CCYDGASVNNDETCEQRRAR 20  
 RESULT 5  
 AAB74113  
 ID AAB74113 standard; Peptide; 20 AA.  
 XX  
 AC AAB74113;  
 XX  
 DT 16-MAY-2001 (first entry)  
 DT  
 XX C-terminal truncated C5a peptide #51.  
 DE  
 XX C5a; complement; antibody; bacterial infection; sinusitis;  
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KM wound; anaphylatoxin; sepsis.  
 XX Unidentified.  
 OS  
 XX WO200115731-A1.  
 PN  
 XX 08-MAR-2001.  
 PD  
 XX 31-AUG-2000; 2000WO-US24219.  
 PF  
 XX 31-AUG-1999; 99US-0387671.  
 PR  
 XX (UNMI ) UNIV MICHIGAN.  
 PA  
 XX Ward PA, Huber-Lang M, Sarma V;  
 PI  
 XX WPI; 2001-226665/23.  
 DR  
 XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

PI Ward PA, Huber-Lang M, Sarma V;  
 XX WPI; 2001-226665/23.  
 DR  
 XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.  
 CC  
 SQ Sequence 20 AA;  
 QY  
 DB 1 CCYDGASVNNDETCEQRRAR 20  
 1 CCYDGASVNNDETCEQRRAR 20  
 DB 1 CCYDGASVNNDETCEQRRAR 20  
 RESULT 6  
 AAB74114  
 ID AAB74114 standard; Peptide; 20 AA.  
 XX  
 AC AAB74114;  
 XX  
 DT 16-MAY-2001 (first entry)  
 DT  
 XX C-terminal truncated C5a peptide #52.  
 DE  
 XX C5a; complement; antibody; bacterial infection; sinusitis;  
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KM wound; anaphylatoxin; sepsis.  
 XX Unidentified.  
 OS  
 XX WO200115731-A1.  
 PN  
 XX 08-MAR-2001.  
 PD  
 XX 31-AUG-2000; 2000WO-US24219.  
 PF  
 XX 31-AUG-1999; 99US-0387671.  
 PR  
 XX (UNMI ) UNIV MICHIGAN.  
 PA  
 XX Ward PA, Huber-Lang M, Sarma V;  
 PI  
 XX WPI; 2001-226665/23.  
 DR  
 XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

CC anaphylatoxin.

SQ Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.3e-10;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20  
 |||||  
 DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 7

AAB74116

ID AAB74116 standard; Peptide: 20 AA.

AC AAB74116;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #54.

XX C5a; complement; antibody; bacterial infection; sinusitis;

XX meningitis; respiratory; gastrointestinal; urinary tract infection;

XX wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMT ) UNIV MICHIGAN.

XX PI Ward PA, Huber-Lang M, Sarma V;

XX DR WPI; 2001-226665/23.

XX PT Compositions for treating blood-borne and toxin mediated diseases and

XX treatment of sepsis in humans and other animals comprises anti-C5a

XX antibodies generated against C-terminal truncated C5a peptides -

XX PS Disclosure; Page 30; 84pp; English.

XX CC The present sequence is a C-terminal truncated C5a peptide fragment. The

XX CC present invention relates to an antibody specific for the present

XX CC sequence. The C5a-antibody can be used in a therapeutic composition,

XX CC which is useful for treating a subject suffering from bacterial

XX CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or

XX CC urinary tract infections or infections in wounds. In addition, the C5a

XX CC antibody can be used for treating sepsis. C5a is also known as

XX CC anaphylatoxin.

SQ Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 2.3e-10;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AC AAB74097;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #35.

XX C5a; complement; antibody; bacterial infection; sinusitis;

XX meningitis; respiratory; gastrointestinal; urinary tract infection;

XX wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMT ) UNIV MICHIGAN.

XX PI Ward PA, Huber-Lang M, Sarma V;

XX DR WPI; 2001-226665/23.

XX PS Disclosure; Page 30; 84pp; English.

XX CC The present sequence is a C-terminal truncated C5a peptide fragment. The

XX CC present invention relates to an antibody specific for the present

XX CC sequence. The C5a-antibody can be used in a therapeutic composition,

XX CC which is useful for treating a subject suffering from bacterial

XX CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or

XX CC urinary tract infections or infections in wounds. In addition, the C5a

XX CC antibody can be used for treating sepsis. C5a is also known as

XX CC anaphylatoxin.

XX SQ Sequence 19 AA;

Query Match 95.6%; Score 109; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAA 19  
 |||||  
 DB 1 CCYDGASVNNDETCEQRAA 19

RESULT 9

AAB74120

ID AAB74120 standard; Peptide: 20 AA.

AC AAB74120;

DT 16-MAY-2001 (first entry)

DE Human C5a peptide fragment #7.

XX Human; C5a; complement; antibody; bacterial infection; sinusitis;

XX meningitis; respiratory; gastrointestinal; urinary tract infection;

XX wound; anaphylatoxin; sepsis.

OS Homo sapiens.  
 XX WO200115731-A1.  
 XX PD 08-MAR-2001.  
 XX PF 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.  
XX (UNMI ) UNIV MICHIGAN.  
XX Ward PA, Huber-Lang M, Sarma V;  
XX WPI; 2001-226665/23.  
XX Compositions for treating blood-borne and toxin mediated diseases and  
XX treatment of sepsis in humans and other animals comprises anti-C5a  
XX antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Fig 15; 84pp; English.  
XX  
XX The present sequence is a peptide fragment of human complement component  
XX C5a (the full-length sequence is given in AAB74109). The present  
XX invention relates to an antibody specific for the present sequence. The  
XX C5a-antibody can be used in a therapeutic composition, which is useful  
XX for treating a subject suffering from bacterial infection, e.g.  
XX sinusitis, meningitis, respiratory, gastrointestinal or urinary tract  
XX infections or infections in wounds. In addition, the C5a antibody can  
XX be used for treating sepsis. C5a is also known as anaphylatoxin.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 95.6%; Score 109; DB 22; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.3e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCYDGASVNNDETCEQRAAR 20  
DB 1 CCYDGASVNNDETCEQRAAR 20  
RESULT 10  
AAB74107  
ID AAB74107 standard; Peptide; 20 AA.  
XX AAB74107;  
XX  
XX 16-MAY-2001 (first entry)  
XX  
XX C-terminal truncated C5a peptide #45.  
XX  
XX C5a; complement; antibody; bacterial infection; sinusitis;  
XX meningitis; respiratory; gastrointestinal; urinary tract infection;  
XX wound; anaphylatoxin; sepsis.  
XX  
XX Unidentified.  
XX  
XX WO200115731-A1.  
XX  
XX 08-MAR-2001.  
XX  
XX 31-AUG-2000; 2000WO-US24219.  
XX  
XX 31-AUG-1999; 99US-0387671.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
XX  
XX Ward PA, Huber-Lang M, Sarma V;  
XX WPI; 2001-226665/23.  
XX  
XX Compositions for treating blood-borne and toxin mediated diseases and  
XX treatment of sepsis in humans and other animals comprises anti-C5a  
XX antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Page 30; 84pp; English.  
XX  
XX The present sequence is a C-terminal truncated C5a peptide fragment. The  
XX present invention relates to an antibody specific for the present

CC sequence. The C5a-antibody can be used in a therapeutic composition,  
CC which is useful for treating a subject suffering from bacterial  
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
CC urinary tract infections or infections in wounds. In addition, the C5a  
CC antibody can be used for treating sepsis. C5a is also known as  
CC anaphylatoxin.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 94.7%; Score 108; DB 22; Length 20;  
Best Local Similarity 95.0%; Pred. No. 4.7e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCYDGASVNNDETCEQRAAR 20  
DB 1 CCYDGASVNNDETCEQRAAR 20  
RESULT 11  
AAB74108  
ID AAB74108 standard; Peptide; 20 AA.  
XX AAB74108;  
XX  
XX 16-MAY-2001 (first entry)  
XX  
XX C-terminal truncated C5a peptide #46.  
XX  
XX C5a; complement; antibody; bacterial infection; sinusitis;  
XX meningitis; respiratory; gastrointestinal; urinary tract infection;  
XX wound; anaphylatoxin; sepsis.  
XX  
XX Unidentified.  
XX  
XX WO200115731-A1.  
XX  
XX 08-MAR-2001.  
XX  
XX 31-AUG-2000; 2000WO-US24219.  
XX  
XX 31-AUG-1999; 99US-0387671.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
XX  
XX Ward PA, Huber-Lang M, Sarma V;  
XX WPI; 2001-226665/23.  
XX  
XX Compositions for treating blood-borne and toxin mediated diseases and  
XX treatment of sepsis in humans and other animals comprises anti-C5a  
XX antibodies generated against C-terminal truncated C5a peptides -  
XX  
XX Disclosure; Page 30; 84pp; English.  
XX  
XX The present sequence is a C-terminal truncated C5a peptide fragment. The  
XX present invention relates to an antibody specific for the present  
XX sequence. The C5a-antibody can be used in a therapeutic composition,  
XX which is useful for treating a subject suffering from bacterial  
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
XX urinary tract infections or infections in wounds. In addition, the C5a  
XX antibody can be used for treating sepsis. C5a is also known as  
XX anaphylatoxin.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 94.7%; Score 108; DB 22; Length 20;  
Best Local Similarity 95.0%; Pred. No. 4.7e-10;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCYDGASVNNDETCEQRAAR 20  
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 12  
 AAB74115  
 ID AAB74115 standard; Peptide; 20 AA.  
 XX  
 AC AAB74115;  
 XX  
 DT 16-MAY-2001 (first entry)  
 XX  
 DE C-terminal truncated C5a peptide #53.  
 XX  
 KW C5a; complement; antibody; bacterial infection; sinusitis;  
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KW wound; anaphylatoxin; sepsis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200115731-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000WO-US24219.  
 XX  
 PR 31-AUG-1999; 99US-0387671.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Ward PA, Huber-Lang M, Sarma V;  
 XX  
 DR WPI; 2001-226665/23.  
 XX  
 PT Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 XX  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.  
 CC  
 XX  
 SQ Sequence 20 AA;  
 XX  
 Query Match 93.0%; Score 106; DB 22; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 9.7e-10;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CCYDGASVNNDETCEQRAAR 20  
 DB 1 CCYDGASVNNDETCEGRVVR 20  
 XX  
 RESULT 13  
 AAB74098  
 ID AAB74098 standard; Peptide; 18 AA.  
 XX  
 AC AAB74098;  
 XX  
 DT 16-MAY-2001 (first entry)  
 XX  
 DE C-terminal truncated C5a peptide #36.  
 XX  
 KW C5a; complement; antibody; bacterial infection; sinusitis;  
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KW wound; anaphylatoxin; sepsis.  
 XX  
 OS Unidentified.  
 XX

PN WO200115731-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000WO-US24219.  
 XX  
 PR 31-AUG-1999; 99US-0387671.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Ward PA, Huber-Lang M, Sarma V;  
 XX  
 DR WPI; 2001-226665/23.  
 XX  
 PT Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -  
 XX  
 PS Disclosure; Page 30; 84pp; English.  
 XX  
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.  
 CC  
 XX  
 SQ Sequence 18 AA;  
 XX  
 Query Match 92.1%; Score 105; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.12e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCYDGASVNNDETCEQRA 18  
 DB 1 CCYDGASVNNDETCEGRA 18  
 XX  
 RESULT 14  
 AAB74102  
 ID AAB74102 standard; Peptide; 19 AA.  
 XX  
 AC AAB74102;  
 XX  
 DT 16-MAY-2001 (first entry)  
 XX  
 DE C-terminal truncated C5a peptide #40.  
 XX  
 KW C5a; complement; antibody; bacterial infection; sinusitis;  
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KW wound; anaphylatoxin; sepsis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200115731-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000WO-US24219.  
 XX  
 PR 31-AUG-1999; 99US-0387671.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Ward PA, Huber-Lang M, Sarma V;  
 XX  
 DR WPI; 2001-226665/23.  
 XX  
 PT Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

PS The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

XX Sequence 19 AA;

Query Match 92.1%; Score 105; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCYDGASVNNDETCEQRAAR 20

DB 1 CCYDGASVNNDETCEQRAAR 19

RESULT 15

AA74109  
 ID AAB74109 standard; Peptide; 20 AA.

XX AAB74109;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #47.

XX C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

XX wound; anaphylatoxin; sepsis.

OS Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMT ) UNITIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-22665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

PS The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

XX Sequence 20 AA;

Query Match 89.5%; Score 102; DB 22; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e-09;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20

DB 1 CCYDGASVNNDETCEQRAAR 20

Search completed: December 9, 2003, 14:14:12  
 Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 9, 2003, 14:12:09 ; Search time 34 Seconds  
(without alignments)  
151.796 Million cell updates/sec

Title: US-09-651-685A-5

Perfect score: 114  
Sequence: 1 CCYDGASVNDTECFQRAAR 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	24.6	19	11 Q9QVJ9	Q9QVJ9 mus sp. mep
2	26	22.8	16	6 Q8SPT4	Q8SPT4 macaca mlla
3	26	22.8	17	15 Q78381	Q78381 human immun
4	26	22.8	18	6 Q46665	Q46665 macropus ro
5	26	22.8	19	4 Q9UCD0	Q9UCD0 homo sapien
6	26	22.8	19	11 Q9QW83	Q9QW83 rattus norv
7	25	21.9	15	4 Q9UCD0	Q9UCD0 homo sapien
8	24	21.1	18	6 Q9T781	Q9T781 dos laurus
9	24	21.1	20	4 Q16188	Q16188 homo sapien
10	24	21.1	20	5 P82201	P82201 bombyx mori
11	23	20.2	16	4 Q81WX4	Q81WX4 homo sapien
12	23	20.2	18	2 Q9RAF3	Q9RAF3 brachyrihob
13	23	20.2	18	2 Q30888	Q30888 brachyrihob
14	23	20.2	18	6 Q97668	Q97668 equus cabal
15	23	20.2	19	2 Q98511	Q98511 brevbacter
16	23	20.2	20	4 Q9UDF5	Q9UDF5 homo sapien

17	22.5	19.7	16	2 Q47605	Q47605 escherichia
18	22.5	19.7	17	5 Q816R5	Q816R5 conus imper
19	22	19.3	10	2 P96421	P96421 neisseria g
20	22	19.3	12	12 Q85666	Q85666 reovirus (t
21	22	19.3	15	11 Q9QV86	Q9QV86 rattus sp.
22	22	19.3	15	11 Q9QV87	Q9QV87 rattus sp.
23	22	19.3	17	5 Q816R4	Q816R4 conus imper
24	22	19.3	18	4 Q9UM83	Q9UM83 homo sapien
25	22	19.3	18	6 Q95MX1	Q95MX1 syncerus ca
26	22	19.3	18	6 Q95MX8	Q95MX8 oryx dammah
27	22	19.3	18	6 Q95MX0	Q95MX0 tragelaphus
28	22	19.3	18	6 Q95MX5	Q95MX5 raphicerus
29	22	19.3	18	6 Q95MW7	Q95MW7 hippobos
30	22	19.3	18	6 Q95MW1	Q95MW1 kobus leche
31	22	19.3	18	6 Q95MW3	Q95MW3 redunda ful
32	22	19.3	18	6 Q95MW5	Q95MW5 alcelaphus
33	22	19.3	18	6 Q95MW0	Q95MW0 pelea capre
34	22	19.3	18	6 Q95MW4	Q95MW4 neotragus m
35	22	19.3	18	6 Q95MW6	Q95MW6 beaureagus h
36	22	19.3	18	6 Q95MW4	Q95MW4 connochaete
37	22	19.3	18	6 Q95MW2	Q95MW2 redunda red
38	22	19.3	18	6 Q95MW8	Q95MW8 litocranius
39	22	19.3	18	6 Q95MW9	Q95MW9 antilocapra
40	22	19.3	18	6 Q95MW2	Q95MW2 cephalopis
41	22	19.3	18	6 Q95MW1	Q95MW1 sylvicapra
42	22	19.3	18	6 Q95MW3	Q95MW3 oreotragus
43	22	19.3	18	6 Q95MW7	Q95MW7 raphicerus
44	22	19.3	18	6 Q95MW0	Q95MW0 ourebia our
45	22	19.3	18	6 Q95MW6	Q95MW6 raphicerus

## ALIGNMENTS

RESULT 1	Q9QVJ9	PRELIMINARY;	PRT;	19 AA.
AC Q9QVJ9				
DT 01-MAY-2000 (TEMBLrel. 13, Created)				
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)				
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)				
DE Mepin-B peptide B1 (Fragment).				
OS Mus sp.				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;				
OX NCBI_Taxid=10095;				
RN [1]				
RP SEQUENCE.				
RX MEDLINE=9137354; PubMed=1894622;				
RA Kounnas M.Z., Wolf R.L., Gorbea C.M., Bond J.S.;				
RT "Mepin-A and -B. Cell surface endopeptidases of the mouse kidney.";				
RL J. Biol. Chem. 266:17350-17357(1991).				
FT NON TER	1	19		
FT NON TER	1	19		
SO SEQUENCE	19 AA;	2157 MW;	81E66F19417E20C5 CRC64;	
Query Match	24.6%;	Score 28;	DB 11;	Length 19;
Best Local Similarity	36.4%;	Pred. No. 8.9e+02;		
Matches	4;	Conservative	4;	Mismatches 3;
				Indels 0;
				Gaps 0;
Qy	3 YDGASVNDDET 13			
Db	1 FNVYSITNDT 11			
RESULT 2				
ID Q8SPT4	PRELIMINARY;	PRT;	16 AA.	
AC Q8SPT4				
DT 01-JUN-2002 (TEMBLrel. 21, Created)				
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)				
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)				
DE Chloride channel 2 (Fragment).				

```

GN CLCN2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Norgren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
RT "Construction of a targeted rhesus macaque microarray."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF498851; AAC9695.1; -.
FT NON TER
SQ SEQUENCE 16 AA; 1691 MW; 50D83BF4FC6AF49E CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 6; Length 16;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGASVNDTCR 15
Db 5 EGSPSDSDCKQ 16

RESULT 3
078381 PRELIMINARY; PRT; 17 AA.
ID Q78381.
AC Q78381.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Viral sample FLPR5F (Florida patient B), partial env cds, VS region
DE (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
RA Kober B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Bonomou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92126; AAA44496.1; -.
FT NON TER
SQ SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 15; Length 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GASVNDDET 13
Db 2 GNNNTTET 10

RESULT 4
046665 PRELIMINARY; PRT; 18 AA.
ID 046665.
AC 046665.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
GN G6PD.
OS Macropus robustus robustus.

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the
RT wallaroo (Macropus robustus) by polymerase chain reaction."
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53775; AAC48790.1; -.
DR InterPro; IPR001282; G6PD.
DR Pfam; PF02781; G6PD_C; 1.
FT NON TER
SQ SEQUENCE 18 AA; 1992 MW; C6D5981B528256FB CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 6; Length 18;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 ASVNDTCRGR 17
Db 7 ASTNSDVRDER 18

RESULT 5
09UCD0 PRELIMINARY; PRT; 19 AA.
ID 09UCD0.
AC 09UCD0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE C215 antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94043256; PubMed=7693697;
RA Bjork P., Jonsson U., Svedberg H., Larsson K., Lind P., Dillner J.,
RA Hedlund G., Dohlsten M., Kalland T.;
RT "Isolation, partial characterization, and molecular cloning of a human
RT colon adenocarcinoma cell-surface glycoprotein recognized by the C215
RT mouse monoclonal antibody."
RL J. Biol. Chem. 268:24232-24241(1993).
SQ SEQUENCE 19 AA; 2042 MW; 54135D12119705B6 CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 4; Length 19;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVND 11
Db 4 EGALQND 11

RESULT 6
09QW83 PRELIMINARY; PRT; 19 AA.
ID 09QW83.
AC 09QW83.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PHOSPHORYLASE-PEPTIDE Fragment 12-44 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91291127; PubMed=2064607;

```

RA Sabsey B., Stecler-Stevenson W.G., Lechner J.H., Veis A.;  
 RT "Domain structure and sequence distribution in dentin phosphoporyn";  
 RL Biochem. J. 276:699-707(1991).  
 DR HSSP; P00760; IAQ7.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2195 MW; 744603FE729FDE0C CRC64;

Query Match 22.8%; Score 26; DB 11; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YDGASVYND 11  
 ID 1: : : : :  
 DB 7 YNSNTLND 15

## RESULT 7

Q9UCCO PRELIMINARY; PRT; 15 AA.

AC Q9UCCO;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Insulin-like growth factor receptor alpha subunit (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94079885; PubMed=8257688;  
 RA Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,  
 RA Fujita-Yamaguchi Y.;  
 RT "Characterization of human placental insulin-like growth factor-  
 RT I/Insulin hybrid receptors by protein microsequencing and  
 RT purification."  
 RL Biochemistry 32:13531-13536(1993).  
 SQ SEQUENCE 15 AA; 1721 MW; 98BC151D6D81784B CRC64;

Query Match 21.9%; Score 25; DB 4; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVYND 11  
 ID 1: : : : :  
 DB 3 CGPGDIRND 12

## RESULT 8

Q9TT81 PRELIMINARY; PRT; 18 AA.

AC Q9TT81;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Wilm's tumor protein 1 (Fragment).  
 GN Wt1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21015404; PubMed=11330975;  
 RA Brouillette J.A., Andrew J.R., Venta P.J.;  
 RT "Sequencing of nucleotide diversity in dogs with a pool-and-sequence  
 RT method";  
 RL Mamm. Genome 11:1079-1086(2000).  
 DR EMBL; AF201738; AAF19824.1; -;  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18

SQ SEQUENCE 18 AA; 2196 MW; 1B58DAD8E072C0BF CRC64;  
 Query Match 21.1%; Score 24; DB 6; Length 18;  
 Best Local Similarity 33.3%; Pred. No. 4e+03;  
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 12 ETCEQAPAR 20  
 ID 1: : : : :  
 DB 7 KTCQRKFSR 15

## RESULT 9

Q16188 PRELIMINARY; PRT; 20 AA.

AC Q16188;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Adenosine deaminase protein (Fragment).  
 GN ADENOSINE DEAMINASE.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94327968; PubMed=8051429;  
 RA Shovlin C.L., Simmonds H.A., Fairbanks L.D., Deacock S.U.,  
 RA Hughes U.M., Lechner R.I., Webster A.D., Sun X.M., Webb J.C.,  
 RA Soutar A.K.;  
 RT "Adult onset immunodeficiency caused by inherited adenosine deaminase  
 RT deficiency";  
 RL U. Immunol. 153:2331-2339(1994).  
 DR EMBL; S72469; AAD14102.1; -;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 20 AA; 2175 MW; 4EABA6143F739B4C CRC64;

Query Match 21.1%; Score 24; DB 4; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 TCQBPAPAR 20  
 ID 1: : : : :  
 DB 12 SCEVRCR 19

## RESULT 10

P82201 PRELIMINARY; PRT; 20 AA.

AC P82201;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=XINZHANG X KEMING, TISSUE=Body wall, and Fat body;  
 RX MEDLINE=21177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of  
 RT silkworm";  
 RL I Chuan Hsueh Pao 28:217-224(2001).  
 CC -I-SIMILARITY: TO THE N-TERMINAL OF TROPOMYOSIN.  
 FT NON\_TER 20 20  
 FT NON\_TER 20 20

SQ SEQUENCE 20 AA; 2215 MW; A3C1EPD3F1350767 CRC64;

Query Match 21.1%; Score 24; DB 5; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 GEORA 18  
| | | |

Db 5 CEOQA 9

# RESULT 11

Q81WX4

ID Q81WX4 PRELIMINARY; PRT; 16 AA.

AC Q81WX4; 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DE Transcription factor AP-2 gamma (Fragment).

GN TFAP2G.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI\_TaxID=9606;

OX (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=22378671; PubMed=12490322;

RA Li M., Wang Y., Yu Y., Nishizawa M., Nakajima T., Ito S., Kannan P.;

RT "The human transcription factor activation protein-2 gamma (AP-2 gamma): gene structure, promoter, and expression in mammary carcinoma cell lines."

RL Gene 301:43-51(2002).

DR EMBL; AF544986; AAN37906.1; -.

FT NON TER 16

SO SEQUENCE 16 AA; 2016 MW; F88CABF56BFC601 CRC64;

Query Match 20.2%; Score 23; DB 4; Length 16;

Best Local Similarity 44.4%; Pred. No. 5.2e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 SYNNDETCE 15  
: | : | |

Db 8 NVKYEEDCE 16

# RESULT 12

Q9R4F3

ID Q9R4F3 PRELIMINARY; PRT; 18 AA.

AC Q9R4F3; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 20 kDa fibrial adhesin subunit (Fragment).

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OC NCBI\_TaxID=562;

OX (1)

RP SEQUENCE.

RX MEDLINE=96110952; PubMed=8557360;

RA Bertin Y., Gizardau J.P., Darfeuille-Michaud A., Contrepois M.;

RT "Characterization of 20k fibrial, a new adhesin of septicemic and diarrhoea-associated Escherichia coli strains, that belongs to a family of adhesins with N-acetyl-D-glucosamine recognition."

RL Infect. Immun. 64:332-342(1996).

FT SEQUENCE 18 AA; 1990 MW; 79AF96A13476DF81 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;

Best Local Similarity 35.7%; Pred. No. 5.9e+03;

Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 YDGASVNNDETCEQ 16  
| | | | : |

Db 1 YDGTINNGKVVQD 14

# RESULT 13

Q30888  
ID Q30888 PRELIMINARY; PRT; 18 AA.

AC Q30888; 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DE Modulation protein (Fragment).

GN MODA.

OS Bradyrhizobium sp.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobiium.

OC NCBI\_TaxID=376;

OX (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=20020861; PubMed=10553291;

RA Steiner J.P., Parker M.A.;

RT "Diversity and relationships of Bradyrhizobia from Amphicarpea RT bractea based on partial nod and ribosomal sequences."

RL Syst. Appl. Microbiol. 22:387-392(1999).

DR EMBL; AF020680; AAB71696.1; -.

FT NON TER 18

SO SEQUENCE 18 AA; 1943 MW; C8C595DCD14D7A5F CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;

Best Local Similarity 28.6%; Pred. No. 5.9e+03;

Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 SYNNDETCEORAR 20  
: | : | |

Db 2 NIPGSRASRSR 15

# RESULT 14

Q97668  
ID Q97668 PRELIMINARY; PRT; 18 AA.

AC Q97668; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE Lactoferrin (Fragment).

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OC NCBI\_TaxID=9796;

OX (1)

RP SEQUENCE FROM N.A.

RA Brandon R.B., Giffard J.M., Bell T.K.;

RT "Isolation of Equine lactoferrin Gene."

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF102025; AAC77463.1; -.

DR HSSP; 077698; ICE2.

DR InterPro; IPR001156; Transferrin.

DR Pfam; PF00405; transferrin; 1.

FT NON TER 18

SO SEQUENCE 18 AA; 1936 MW; D8FBFA226A6DD9 CRC64;

Query Match 20.2%; Score 23; DB 6; Length 18;

Best Local Similarity 66.7%; Pred. No. 5.9e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGA 6  
| | | |

Db 1 CLQDGA 6

# RESULT 15

Q9RS11  
ID Q9RS11 PRELIMINARY; PRT; 19 AA.

AC Q9RS11; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Nitrite hydratase alpha subunit (Fragment).  
OS Brevibacterium.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococciaceae; Brevibacteriaceae.  
OX NCBI\_TaxID=1696;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92407758; PubMed=1527703;  
RA Duran R., Chion C.K., Bigey F., Arnaud A., Galzy P.;  
RT "The N-terminal amino acid sequences of Brevibacterium sp. R312  
RL nitrite hydratase.";  
RL J. Basic Microbiol. 32:13-19(1992).  
SQ SEQUENCE 19 AA; 1923 MW; 84726D1A1282FB63 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 19;  
Best local similarity 50.0%; Pred. No. 6.3e+03;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 7 SVNNDETCEORA 18  
DB 1 SVTIDHTTNNAA 12

Search completed: December 9, 2003, 14:15:22  
Job time : 35 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 14:09:04 ; Search time 11 Seconds  
(without alignments)  
85.503 Million cell updates/sec

Title: US-09-651-685A-5  
Sequence: 1 CCYDASVNDCECPRAR 20

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	31.5	27.6	16 1 CXAL CONEP	P56638 conus episc
2	29.5	25.9	18 1 CXAL CONEP	P50982 conus ermin
3	29	25.4	15 1 ITRB ALBU	P24927 albizzia ju
4	26	22.8	13 1 CXAA CONST	P28878 conus stria
5	25	21.9	16 1 CXAL CONAL	P56639 conus aulic
6	25	21.9	16 1 CXAA CONEP	P50984 conus penna
7	25	21.9	18 1 HSTB_ECOLI	P01560 escherichia
8	25	21.9	19 1 LCRP_PETVA	P01096 petromyzon
9	24	21.1	14 1 SCCK3_LEIOU	P28661 leiurus qui
10	24	21.1	20 1 SB60_MAIZE	P01521 conus mayi (m
11	23	20.2	14 1 CXAL CONMA	P50983 conus imper
12	22	19.3	12 1 CXAL CONMA	P59072 pseudonaja
13	21	18.4	11 1 NKSXN_PSETE	P59073 pseudonaja
14	21	18.4	15 1 NKSXN_PSETE	P59073 pseudonaja
15	21	18.4	15 1 UNO1_PINS	P51106 pinus pinas
16	21	18.4	16 1 CXAB CONAL	P56641 conus aulic
17	21	18.4	16 1 CXAB CONEP	P50985 conus penna
18	21	18.4	18 1 SC18_MESMA	P14216 limulus pol
19	21	18.4	20 1 SC18_MESMA	P58570 mesobuthus
20	20	17.5	10 1 RRP1_PROVU	P25946 phocine dis
21	20	17.5	11 1 CXSA_CONAL	P58848 conus aulic
22	20	17.5	11 1 CXSB_CONAL	P58849 conus aulic
23	20	17.5	13 1 CXAZ_CONEP	P01520 conus geogr
24	20	17.5	14 1 CXA1_CONEP	P58623 conus betul
25	20	17.5	14 1 CXA1_CONEP	P56973 conus conso
26	20	17.5	15 1 CXB1_CONEP	P56624 conus betul
27	20	17.5	15 1 CXB1_CONEP	P1285 mamestra bt
28	20	17.5	15 1 TERN_BPM2	P19897 bacterioph
29	20	17.5	16 1 FOK1_MYRDU	P21438 myrmecia gu
30	20	17.5	17 1 TAC1_TACGI	P23684 tachyples
31	20	17.5	17 1 TAC3_TACGI	P18253 tachyples
32	20	17.5	18 1 PPM1_LIMPO	P14215 limulus pol
33	20	17.5	19 1 HIT0_RAT	P21794 ratus norv

34	19	16.7	9 1 OXYA_SCYCA	P42996 scyllorhinu
35	19	16.7	9 1 OXYA_SOUAC	P42999 squallus aca
36	19	16.7	10 1 COXA_ONCMY	P80328 oncorhynch
37	19	16.7	10 1 PRCK_FASHE	P80525 faeciola he
38	19	16.7	10 1 UH05_RAT	P56573 ratius norv
39	19	16.7	15 1 ARCD_PSEPU	P55936 didelphis m
40	19	16.7	16 1 ARCD_PSEPU	P41147 pseudomona
41	19	16.7	17 1 CXMA_CONEP	P58926 conus penna
42	19	16.7	17 1 CXMB_CONEP	P58927 conus penna
43	19	16.7	17 1 PATS_ANASP	P52748 anabaena sp
44	19	16.7	18 1 RL24_PROVU	P20032 proteus vul
45	19	16.7	18 1 UC03_MAIZE	P80609 zea mays (m

## ALIGNMENTS

RESULT 1				
ID	CXAL CONEP	STANDARD;	PRT;	16 AA.
AC	P56638;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Alpha-conotoxin Epi.			
OS	Conus episcopatus (Bishop's cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC	Apogastropoda; Caenogastropoda; Sorbeconcha; Hypogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxId=88764;			
RN	[1]			
RP	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).			
RX	MEDLINE=96376423; PubMed=9708977;			
RA	Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,			
RA	Alewood P.F., Lewis R.J., Martin J.L.;			
RT	"The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel			
RT	alpha-conotoxin from Conus episcopatus, solved by direct methods."			
RL	Biochemistry 37:11425-11433(1998).			
CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY			
CC	BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS			
CC	INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC			
CC	ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-			
CC	3/BETA-4 SUBUNITS.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	-1- SIMILARITY: BELONGS TO THE A-SUBFAMILY OF CONOTOXINS. ALPHA-TYPE			
CC	FAMILY.			
DR	PIR; A59042; A59042.			
DR	PDB; 1A0M; 13-JAN-99.			
KW	Postsynaptic neurotoxin; Neurotoxin; Toxin;			
KW	Acetylcholine receptor inhibitor; Amidation;			
KW	Sulfation; 3D-structure.			
FT	DISULFID	2	8	
FT	DISULFID	3	16	
FT	MOD_RES	15	15	SULFATION.
FT	MOD_RES	16	16	AMIDATION.
FT	HELI	2	4	
FT	HELI	6	11	
FT	TURN	13	16	
SO	SEQUENCE	16 AA; 1792 MM;		C63385F376C99B4C CRC64;
QY	Query Match	27.6%;	Score 31.5; DB 1; Length 16;	
QY	Best local Similarity	40.0%;	Pred. No. 43;	
QY	Matches	6; Conservative	3; Mismatches	5; Indels 1; Gaps 1;
DB	1 CCYD-GASVNDCEC 14			
DB	2 CCSDPRCMMNPVC 16			
RESULT 2				
ID	CXAL CONEP	STANDARD;	PRT;	18 AA.

AC P50982; 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin EI.  
 OS Conus ermineus (Atlantic fish-hunting cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_Taxid=55423;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=96062516; PubMed=7578057;  
 RA Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Grebe D.R.,  
 RA Abramson S.N., McIntosh J.M.;  
 RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor  
 antagonist with novel selectivity.";  
 RL Biochemistry 34:14519-14526(1995).  
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 INHIBIT THEM.  
 CC -1- SUBUNIT: Binds nicotinic acetylcholine receptor.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
 FAMILY.  
 DR PIR: A58589;  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; Hydroxylation.  
 FT DISULFID 4 10  
 FT MOD\_RES 5 18  
 FT MOD\_RES 3 3  
 FT MOD\_RES 18 18  
 FT MOD\_RES 18 18  
 SQ SEQUENCE 18 AA; 2082 MW; 60A61AC427A655E CRC64;  
 Query Match 25.9%; Score 29.5; DB 1; Length 18;  
 Best Local Similarity 33.3%; Pred. No. 1e+02;  
 Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 CCY-DGASVNNDETC 14  
 DB 4 CCHPTCMSNPQIC 18  
 RESULT 3  
 ID TRRB\_ALBUJ STANDARD; PRT; 15 AA.  
 AC P24927;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Trypsin inhibitor B chain (Fragment).  
 OS Albizzia julibrissin (Silk tree).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizzia.  
 OX NCBI\_Taxid=3813;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RX MEDLINE=80115605; PubMed=528539;  
 RA Odani S., Ono T., Ikenaka T.;  
 RT "Proteinase inhibitors from a mimosoideae legume, Albizzia  
 julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";  
 RL J. Biochem. 86:1795-1805(1979).  
 CC -1- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.  
 CC -1- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A  
 DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR  
 FAMILY.  
 KW Serine protease inhibitor.  
 FT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;  
 Query Match 25.4%; Score 29; DB 1; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 1e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 CYDGASVNNDE 12  
 DB 5 CKDLGSDIDDE 15  
 RESULT 4  
 ID CXAA\_CONST STANDARD; PRT; 13 AA.  
 AC P28878;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin S1A (S1A).  
 OS Conus striatus (Striated cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_Taxid=6493;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=91369955; PubMed=1892838;  
 RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,  
 RA Olivera B.M.;  
 RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine  
 receptors.";  
 RL Biochemistry 30:9370-9377(1991).  
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 INHIBIT THEM.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
 FAMILY.  
 DR PIR: A40312; NTKNAS.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 7  
 FT DISULFID 3 13  
 FT MOD\_RES 13 13  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;  
 Query Match 22.8%; Score 26; DB 1; Length 13;  
 Best Local Similarity 36.4%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 CCYDGASVNNDE 11  
 DB 2 CCHPACGKNFID 12  
 RESULT 5  
 ID CXAL\_CONAL STANDARD; PRT; 16 AA.  
 AC P56639;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin A1A.  
 OS Conus aulicus (Cone cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_Taxid=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;

RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Oliveira B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin Aurb selectively blocks alpha4 beta4 nicotinic  
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC  
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.  
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
 CC FAMILY.  
 DR PIR; A59045; A59045.  
 DR HSSP; P50984; IPEN.  
 DR Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KM Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT MOD\_RES 3 16  
 FT MOD\_RES 16 16  
 SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 16;  
 Best Local Similarity 28.6%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCYDGASVNDCTC 14  
 Db 3 CSEPCPATNSDYC 16

## RESULT 6

ID CXXA CONPE STANDARD; PRT; 16 AA.  
 AC P50984;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin PnIA.  
 OS Conus pennaceus (feathered cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbococoncha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OC NCBI\_TaxID=37335;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=94347719; PubMed=8068627;  
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,  
 RA Spira M.E., Zlotkin E.;  
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal  
 RT acetylcholine receptors.";  
 RL Biochemistry 33:9523-9529(1994).  
 RN [2]  
 RP SULFATION OF TYR-15.  
 RX MEDLINE=99242956; PubMed=10226369;  
 RA Wolender J.L., Chu F., Ball H., Wolender F., Fainzilber M.,  
 RA Balwin M.A., Burlingame A.L.;  
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins  
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and  
 RT phosphopeptides by electrospray, matrix-assisted laser  
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass  
 RT spectrometry.";  
 RL J. Mass Spectrom. 34:447-454(1999).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).  
 RX MEDLINE=96311277; PubMed=8740364;  
 RA Hu S.-H., Gehmann U., Gaddat L.W., Alewood P.F., Craik D.J.,  
 RA Martin J.L.;  
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor  
 RT antagonist, alpha-conotoxin PnIA from Conus pennaceus.";

RL Structure 4:417-423(1996).  
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE  
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS  
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
 CC FAMILY.  
 DR PIR; A54877; A54877.  
 DR PDB; IPEN; 2I-APR-97.  
 DR Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KM Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.  
 FT DISULFID 2 8  
 FT MOD\_RES 15 15  
 FT MOD\_RES 16 16  
 FT MOD\_RES 16 16  
 FT HELIX 2 4  
 FT HELIX 6 11  
 FT TURN 13 16  
 SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 16;  
 Best Local Similarity 28.6%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCYDGASVNDCTC 14  
 Db 3 CSEPCPATNSDYC 16

## RESULT 7

ID HSTB ECOLI STANDARD; PRT; 18 AA.  
 AC P01560;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Heat-stable enterotoxin ST-2 (ST-B).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=O42:K86:H37 / 18D;  
 RX MEDLINE=81264141; PubMed=7021541;  
 RA Chan S.-K., Giannella R.A.;  
 RT "Amino acid sequence of heat-stable enterotoxin produced by  
 RT Escherichia coli pathogenic for man.";  
 RL J. Biol. Chem. 256:7744-7746(1981).  
 RN [2]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=87191003; PubMed=3552731;  
 RA Shimomichi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,  
 RA Miwatani T., Takeda Y.;  
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STb)  
 RT produced by a human strain of enterotoxigenic Escherichia coli.";  
 RL FEBS Lett. 215:165-170(1987).  
 CC -1- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE  
 CC CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST  
 CC INTESTINAL EPITHELIAL CELLS.  
 CC -1- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE  
 CC PRODUCED BY PATHOGENIC STRAINS OF E.COLI AND AFFECT THE DIGESTIVE  
 CC TRACT OF MAMMALS.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.  
 DR PIR; A01823; CHECC.  
 DR HSSP; P01559; 1ETN.  
 DR InterPro; IPR001489; Enterotoxin HS.  
 DR Pfam; PF02048; Enterotoxin HS; 1\_  
 DR POSITIVE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
 KM Toxin; Enterotoxin.



FT DISULFID 5 10  
 FT DISULFID 6 14  
 FT DISULFID 9 17  
 SQ SEQUENCE 18 AA; 1978 MW; D0C975F49D600650 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3  
 DB 9 CCY 11

RESULT 8  
 LCRP\_PETMA STANDARD; PRT; 19 AA.  
 ID LCRP\_PETMA  
 AC 010956;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Corticostatin-related protein LCRP.  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 NCBI\_TaxID=7757;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=96321324; PubMed=8759287;  
 RA Conlon J.M., Sower S.A.;  
 RT "Isolation of a peptide structurally related to mammalian  
 RT corticostatins from the lamprey Petromyzon marinus."  
 RL Comp. Biochem. Physiol. 114B:133-137(1996).  
 CC -1- FUNCTION: MAY HAVE MICROBICIDAL ACTIVITIES. MAY INHIBIT  
 CC CORTICOTROPIN (ACTH) STIMULATED STEROIDOGENESIS AND THE MICROBIAL  
 CC ACTIONS OF THE CORTICOSTATINS.  
 CC -1- MASS SPECTROMETRY: MW=2201; MW ERR=0.4; METHOD=Electrospray.  
 CC -1- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.  
 KW Defensin; Antibiotic.  
 FT DISULFID 1 18 BY SIMILARITY.  
 FT DISULFID 3 9 BY SIMILARITY.  
 FT DISULFID 8 17 BY SIMILARITY.  
 SQ SEQUENCE 19 AA; 2209 MW; 8D9CDBCT1A19A85 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 5.7e+02;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCYDASV 8  
 DB 8 CCVRGLNV 15

RESULT 9  
 SCK3\_LEIQU STANDARD; PRT; 14 AA.  
 ID SCK3\_LEIQU  
 AC P45661;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leituruxin III (Fragment).  
 OS Leituruxin quinquestratus quinquestratus (Egyptian scorpion).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Butioidae; Butiidae; Leiturux.  
 NCBI\_TaxID=6885;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=93075256; PubMed=1280139;  
 RA Valdivia H.H., Martin B.M., Escobar L., Possani L.D.;  
 RT "Noxiustoxin and leituruxin III, two homologous peptide toxins with  
 RT binding properties to synaptosomal membrane K<sup>+</sup> channels."

RL Biochem. Int. 27:953-962(1992).  
 CC -1- FUNCTION: Blocker of potassium channels.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM  
 CC CHANNEL INHIBITORS SUBFAMILY.  
 CC PIR: A48389; A48389.  
 DR InterPro: IPR001947; Scorpion toxins.  
 DR PROSITE: PS01138; SCORP\_SHORT\_TOXIN; PARTIAL.  
 KW Toxin; Neurotoxin; Ionic channel inhibitor;  
 KW Potassium channel inhibitor.  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1588 MW; 83C67CCBD691205E CRC64;

Query Match 21.1%; Score 24; DB 1; Length 14;  
 Best Local Similarity 35.7%; Pred. No. 5.9e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

OY 2 CYDASVNDNCE 15  
 DB 7 CYDSSQ-----CE 14

RESULT 10  
 SB60\_MAIZE STANDARD; PRT; 20 AA.  
 ID SB60\_MAIZE  
 AC P82866;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative 60 kDa spermidine-binding protein (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE. AND SUBCELLULAR LOCATION.  
 RC STRAIN=cv. Cecilia; TISSUE=Coleoptile;  
 RX MEDLINE=21948208; PubMed=11950979;  
 RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;  
 RT "Spermidine-binding proteins. Purification and expression analysis in  
 RT maize."  
 RT Plant Physiol. 128:1303-1312(2002).  
 CC -1- FUNCTION: May have spermidine-binding activity.  
 CC -1- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).  
 CC -1- SUBCELLULAR LOCATION: Microsomal membrane.  
 CC -1- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.  
 DR GO: GO:0005792; C:mitosome; NAS.  
 KW Membrane; Mitosome.  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2093 MW; 7FD730C00391579A CRC64;

Query Match 21.1%; Score 24; DB 1; Length 20;  
 Best Local Similarity 40.0%; Pred. No. 8.7e+02;  
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 6 ASVNDTECORAR 20  
 DB 4 AVEPEPTSORRIAK 18

RESULT 11  
 CXAI\_CONMA STANDARD; PRT; 14 AA.  
 ID CXAI\_CONMA  
 AC P01521;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin MI (MI).  
 OS Conus magus (Magus cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypoastropoda;

CC Neogastrópoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=6492;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83073458; PubMed=7149738;  
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;  
RT "Isolation and structure of a peptide toxin from the marine snail  
RT Conus maurus";  
RL Arch. Biochem. Biophys. 218:329-334(1982).  
RN [2]  
RP DISULFIDE BONDS.  
RX MEDLINE=84032400; PubMed=6630187;  
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;  
RT "Conotoxin M1. Disulfide bonding and conformational states";  
RL J. Biol. Chem. 258:12247-12251(1983).  
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
CC INHIBIT THEM.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
DR PIR; A01784; NTRN1M.  
DR HSSP; P56973; 1845.  
KM Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KM Acetylcholine receptor inhibitor; Amidation.  
FT DISULFID 3 8  
FT DISULFID 4 14  
FT MOD RSS 14 14  
SQ SEQUENCE 14 AA; 1499 MW; DEER91898BPS5ESBD CRC64;  
  
Query March 20.2%; Score 23; DB 1; Length 14;  
Best Local Similarity 33.3%; Pred. No. 8.5e+02;  
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 CCYDASYN 9  
DB 3 CCHPACGKN 11  
  
RESULT 12  
CXAL CONTM STANDARD; PRT; 12 AA.  
AC P50983;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Alpha-conotoxin Imi.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Neogastrópoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastrópoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE=Venom.  
RX MEDLINE=94266889; PubMed=8206995;  
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,  
RA Gray W.R., Olivera B.M.;  
RT "A nicotinic acetylcholine receptor ligand of unique specificity,  
RT alpha-conotoxin Imi";  
RL J. Biol. Chem. 269:16733-16739(1994).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=95379776; PubMed=7651351;  
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,  
RA McIntosh J.M.;  
RT "Alpha-conotoxin Imi exhibits subtype-specific nicotinic  
RT acetylcholine receptor blockade: preferential inhibition of homomeric  
RT alpha 7 and alpha 9 receptors";  
RL Mol. Pharmacol. 48:194-199(1995).  
RN [3]  
RP STRUCTURE BY NMR.

RX MEDLINE=99212205; PubMed=10194298;  
RA Rogers J.P., Luginduhl P., Shen G.S., McCabe R.T., Stevens R.C.,  
RA Memmer D.E.;  
RT "NMR solution structure of alpha-conotoxin Imi and comparison to  
RT other conotoxins specific for neuronal nicotinic acetylcholine  
RT receptors";  
RL Biochemistry 38:3874-3882(1999).  
RN [4]  
RP STRUCTURE BY NMR.  
RX MEDLINE=99280313; PubMed=10350614;  
RA Gouda H., Hirono S.;  
RT "Solution structure of alpha-conotoxin Imi determined by  
RT two-dimensional NMR spectroscopy";  
RL Biochim. Biophys. Acta 1431:384-394(1999).  
RN [5]  
RP STRUCTURE BY NMR.  
RX MEDLINE=99158061; PubMed=10050774;  
RA Malenkov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,  
RA Methfessel C., Tsetlin V.I., Arseniev A.S.;  
RT "NMR spatial structure of alpha-conotoxin Imi reveals a common  
RT scaffold in snail and snake toxins recognizing neuronal nicotinic  
RT acetylcholine receptors";  
RL FEBS Lett. 444:275-280(1999).  
RN [6]  
RP STRUCTURE BY NMR.  
RX MEDLINE=99358772; PubMed=10431825;  
RA Lanthanh H., Jegou-Mathéron C., Servent D., Menez A., Lancelin J.-M.;  
RT "Minimal conformation of the alpha-conotoxin Imi for the alpha7  
RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,  
RT NMR and binding studies";  
RL FEBS Lett. 454:293-298(1999).  
RN [7]  
RP STRUCTURE BY NMR.  
RX MEDLINE=99324017; PubMed=10395477;  
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;  
RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic  
RT resonance";  
RL J. Med. Chem. 42:2364-2372(1999).  
RN [8]  
RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE  
RP THREE MUTANTS.  
RX MEDLINE=20574023; PubMed=11124036;  
RA Rogers J.P., Luginduhl P., Pemberton K., Hartly P., Memmer D.E.,  
RA Stevens R.C.;  
RT "Structure-activity relationships in a peptidic alpha7 nicotinic  
RT acetylcholine receptor antagonist";  
RL J. Mol. Biol. 304:911-926(2000).  
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
CC bind to the nicotinic acetylcholine receptors (NACHR) and thus  
CC inhibit them. It is highly active against the neuromuscular  
CC receptor in frog but not in mice. In contrast, it induces seizures  
CC when injected centrally in mice and rats. It targets neuronal  
CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors  
CC with the highest apparent affinity and homomeric alpha-9 receptors  
CC with 8-fold lower affinity. It has no effect on receptors composed  
CC of alpha-2/beta-2, or alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,  
CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
DR PIR; A53709; A53709.  
DR PDB; 1IM1; 15-JUN-99.  
DR PDB; 1IM1; 23-APR-99.  
DR PDB; 1CNI; 27-MAY-99.  
DR PDB; 1E74; 27-DEC-00.  
DR PDB; 1E75; 27-DEC-00.  
DR PDB; 1E76; 27-DEC-00.  
DR PDB; 1G2G; 08-NOV-00.  
KM Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KM Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
FT DISULFID 2 8  
FT DISULFID 3 12

FT MOD RES 12 12 AMINATION.  
 FT MUTAGEN 5 5 D->I: REDUCTION OF TOXICITY.  
 FT MUTAGEN 7 7 R->L: REDUCTION OF TOXICITY.  
 FT MUTAGEN 11 11 R->E: NO LOSS OF ACTIVITY.  
 FT HELIX 2 4  
 FT TURN 6 8  
 FT TURN 10 12  
 SO SEQUENCE 12 AA; 1357 MW; 9C29CEA545A176A CRC64;

Query Match 19.3%; Score 22; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYD 4  
 DB 2 CCSD 5

RESULT 13  
 NXSX\_PSETTE STANDARD; PRT; 11 AA.  
 AC P59072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
 OC Pseudonaja textilis (Eastern brown snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Elapidae; Squamata; Scleroglossa; Serpentes; Colubroides;  
 OC Elapidae; Acanthophinae; Pseudonaja.  
 OX NCBI\_TaxID=8673;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99449602; PubMed=10518793;  
 RA Gong N.L., Armugam A., Jeyaseelan K.;  
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
 RT cloning, expression and protein characterization.";  
 RL Eur. J. Biochem. 265:982-989(1999).  
 CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
 CC acetylcholine receptors (nAChR).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- MASS SPECTROMETRY: MM=6236; METHOD=Electrospray.  
 CC -1- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
 CC -1- SIMILARITY: Belongs to the snake toxin family.  
 CC -1- SIMILARITY: Belongs to the snake toxin family.  
 DR InterPro: IPR003571; Snake toxin.  
 DR PROSITE: PS00272; SNAKE\_TOXIN; PARTIAL.  
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
 KW Acetylcholine receptor inhibitor; Multigene family.  
 FT UNSURE  
 FT NON\_TER  
 SO SEQUENCE 15 AA; 1727 MW; E149FD4BFD1EF0DD CRC64;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
 OC Elapidae; Acanthophinae; Pseudonaja.  
 OX NCBI\_TaxID=8673;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99449602; PubMed=10518793;  
 RA Gong N.L., Armugam A., Jeyaseelan K.;  
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
 RT cloning, expression and protein characterization.";  
 RL Eur. J. Biochem. 265:982-989(1999).  
 CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
 CC acetylcholine receptors (nAChR).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- MASS SPECTROMETRY: MM=6345; METHOD=Electrospray.  
 CC -1- MISCELLANEOUS: LD(50) is 0.80 mg/kg by intravenous injection.  
 CC -1- SIMILARITY: Belongs to the snake toxin family.  
 DR InterPro: IPR003571; Snake toxin.  
 DR PROSITE: PS00272; SNAKE\_TOXIN; PARTIAL.  
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
 KW Acetylcholine receptor inhibitor; Multigene family.  
 FT UNSURE  
 FT NON\_TER  
 SO SEQUENCE 15 AA; 1727 MW; E149FD4BFD1EF0DD CRC64;

Query Match 18.4%; Score 21; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYDG 5  
 DB 3 CYKG 6

RESULT 15  
 UNO1\_PINPS STANDARD; PRT; 15 AA.  
 ID UNO1\_PINPS  
 AC P81106;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Unknown protein from 2D-page of needles (S124/S1248) (N150/N151)  
 DE (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RC Plomion C.; Costa P., Bahman N., Frigerio J.M.;  
 RA "Genetic analysis of needle proteins in maritime pine. 1. Mapping  
 RT dominant and codominant protein markers assayed on diploid tissue, in  
 RT a haploid-based genetic map.";  
 RL Silva Genet. 46:161-165(1997).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RC MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,  
 RA Frigerio J.M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.  
 FT NON\_TER  
 FT NON\_TER  
 SO SEQUENCE 15 AA; 1670 MW; 29CE44CD51B98FCF CRC64;

QY 2 CYDG 5  
 DB 3 CYKG 6

Query Match 18.4%; Score 21; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 66.7%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 SVNDE 12  
| | |  
Db 9 SATNDE 14

Search completed: December 9, 2003, 14:14:36  
Job time : 13 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 9, 2003, 14:12:40 ; Search time 20 Seconds  
(without alignments)  
96.169 Million cell updates/sec

Title: US-09-651-685A-5  
Perfect score: 114  
Sequence: 1 CCYDGASVNNDETCGRAR 20

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.5	27.6	16	2 A59042	alpha-conotoxin Epi
2	29.5	25.9	18	1 A58589	alpha-conotoxin Epi
3	28	24.6	20	2 B44907	manganese peroxidase
4	26	22.8	13	1 NTKNAS	alpha-conotoxin SI
5	25	21.9	16	2 A59045	alpha-conotoxin Au
6	25	21.9	16	2 A54877	alpha-conotoxin Pn
7	25	21.9	18	1 QHEC2	heat-stable entero
8	25	21.9	20	2 PC2248	lambda 112 protein
9	24	21.1	14	2 A48389	leu-enkephalin III -
10	24	21.1	16	2 PD0002	inulin fructotrans
11	23	20.2	12	2 S28215	glucan endo-1,3-be
12	23	20.2	14	1 NTKNIM	alpha-conotoxin MI
13	23	20.2	16	2 PH1317	ig heavy chain DJ
14	23	20.2	17	2 S60171	sex-lethal protein
15	23	20.2	18	2 D49570	plasma membrane ca
16	23	20.2	18	2 B48839	T-cell receptor be
17	23	20.2	19	2 B80226	tyrosin inhibitor
18	23	20.2	20	2 FC1150	equinatoxin IB - B
19	22	19.3	13	2 A53709	factor X activator
20	22	19.3	12	1 A60379	ig heavy chain DJ
21	22	19.3	19	2 PH1330	hypothetical prote
22	22	19.3	20	2 S08605	chromogranin-B - r
23	22	19.3	20	2 H49154	lectin, galactose/
24	22	19.3	20	2 A31516	C6b1 homolog - cha
25	21.5	18.9	13	2 B58553	cytochrome c553 -
26	21	18.4	10	2 PC4442	complement C3b rec
27	21	18.4	11	2 D45900	H+-transporting tw
28	21	18.4	15	2 S49409	ig heavy chain DJ
29	21	18.4	15	2 PH1318	

30	21	18.4	16	2 CS9045	alpha-conotoxin Au
31	21	18.4	16	2 B54877	alpha-conotoxin Pn
32	21	18.4	16	2 H49039	T-cell receptor be
33	21	18.4	16	2 PL0137	protein kinase, 80
34	21	18.4	16	4 I79565	hypothetical TCR3/
35	21	18.4	17	2 I58087	ryanodine receptor
36	21	18.4	18	2 JU0125	polypneumatin II -
37	21	18.4	19	2 C21182	4K prothoracicopro
38	21	18.4	19	2 A21182	4K prothoracicopro
39	21	18.4	19	2 A49254	TCR delta chain V-
40	21	18.4	19	2 S65435	manganese peroxidase
41	21	18.4	20	2 JF0410	bombayxin-IV chain
42	21	18.4	20	2 D25507	proteinase inhibitor
43	21	18.4	20	2 S48746	beta tubulin b-bet
44	20	17.5	8	2 D61512	variant surface gl
45	20	17.5	11	2 S65395	chemical-sense-rel

## ALIGNMENTS

RESULT 1  
A59042  
C/Species: Conus episcopatatus (Bishop's cone)  
C/Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 13-Aug-1999  
C/Accession: A59042  
R/Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.  
J. Biol. Chem. 273, 15667-15674, 1998  
A/Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatatus that selec  
A/Reference number: A59042; PMID:98280307; PMID:9624161  
A/Accession: A59042  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <IOU>  
C/Superfamily: alpha-conotoxin  
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot  
F/1-16/Product: alpha-conotoxin Epi #status experimental <MAT>  
F/1-8,3-16/Dissulfide bonds: #status experimental  
F/15/Binding site: sulfated (Tyr) (covalent) #status experimental  
F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 27.6%; Score 31.5; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
Cy 1 CCYD-GASVNNDETC 14  
Db 2 CCSDPRCMMNNPDTC 16

## RESULT 2

A58589  
C/Species: Conus ermineus (ermine cone)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: A58589  
R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Aramson, S.N.; I  
Biochemistry 34, 14519-14526, 1995  
A/Title: alpha-Conotoxin Epi, a new nicotinic acetylcholine receptor antagonist with nove  
A/Reference number: A58589; PMID:9602516; PMID:7578057  
A/Accession: A58589  
A/Molecule type: protein  
A/Residues: 1-18 <MAR>  
A/Note: sequence confirmed by chemical synthesis  
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt  
C/Superfamily: alpha-conotoxin  
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; post  
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental  
F/4-10,5-18/Dissulfide bonds: #status experimental  
F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.3%; Score 29.5; DB 1; Length 18;

Best Local Similarity 33.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 CCY-DGASVNNDETTC 14

Db 4 CCHPTCMNMNPQC 18

#### RESULT 3

B44907

manganese peroxidase (EC 1.11.1.13) H3 - basidiomycete (Phanerochaete chrysosporium) (F)

C/Species: Phanerochaete chrysosporium

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 06-Dec-1996

C/Accession: B44907

R/Pease, E.A.; Tien, M.

J. Bacteriol. 174, 3532-3540, 1992

A/Title: Heterogeneity and regulation of manganese peroxidases from Phanerochaete chrys

A/Reference number: A44907; MUID:92276331; PMID:1592808

A/Accession: B44907

A/Molecule type: protein

A/Residues: 1-20 <PEA>

A/Experimental source: BKM-F-1767, ATCC 24725

A/Note: sequence extracted from NCBI backbone (NCBIP:104607)

C/Superfamily: lignin peroxidase

C/Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 24.6%; Score 28; DB 2; Length 20;

Best Local Similarity 71.4%; Pred. No. 7.2e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVNN 10

Db 5 DGTGKVN 11

#### RESULT 4

alpha-conotoxin STA - cone shell (Conus striatus)

C/Species: Conus striatus (striated cone)

C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 23-May-1997

C/Accession: A40312

R/Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.

Biochemistry 30, 9370-9377, 1991

A/Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.

A/Reference number: A40312; MUID:9136955; PMID:1892838

A/Accession: A40312

A/Molecule type: protein

A/Residues: 1-13 <MYE>

C/Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F/2-7,3-13/Disulfide bonds: #status experimental

F/13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.8%; Score 26; DB 1; Length 13;

Best Local Similarity 36.4%; Pred. No. 9.8e+02;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCYDGASVNNND 11

Db 2 CCHPACGKNPD 12

RESULT 5

alpha-conotoxin AUIA - cone shell (Conus aulicus)

C/Species: Conus aulicus (court cone)

C/Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999

C/Accession: A59045

R/Liu, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI

J. Neurosci. 18, 8571-8579, 1998

A/Title: Alpha-conotoxin AUIB selectively blocks alpha3beta4 nicotinic acetylcholine rec

A/Accession: A59045

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <UO>

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F/1-16/Product: alpha-conotoxin AUIA #status experimental <MAT>

F/2-8,3-16/Disulfide bonds: #status experimental

F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;

Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETTC 14

Db 3 CSVPPCFATNPDYC 16

#### RESULT 6

alpha-conotoxin PHIA [validated] - cone shell (Conus pennaceus)

N/Alternate names: alpha-CTX-PHIA

C/Species: Conus pennaceus

C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000

C/Accession: A54877

R/Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlocki

Biochemistry 33, 9523-9529, 1994

A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine recei

A/Reference number: A54877; MUID:94347719; PMID:8068627

A/Accession: A54877

A/Molecule type: protein

A/Residues: 1-16 <PAI>

R/Hu, S.H.; Gehrmann, U.; Guddat, L.M.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A/Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F/2-8,3-16/Disulfide bonds: #status experimental

F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;

Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETTC 14

Db 3 CSVPCCANNPDYC 16

#### RESULT 7

CHBC2

heat-stable enterotoxin ST-2 - Escherichia coli

C/Species: Escherichia coli

C/Date: 06-Jul-1982 #sequence\_revision 06-Jul-1982 #text\_change 31-Dec-1996

C/Accession: A01823

R/Chan, S.K.; Giannelis, R.A.

J. Biol. Chem. 256, 7744-7746, 1981

A/Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat

A/Reference number: A01823; MUID:81264141; PMID:7021541

A/Accession: A01823

A/Molecule type: protein

A/Residues: 1-18 <CHA>

C/Experimental source: strain 18D, serotype 0.42:H6:H37

C/Comment: This enterotoxin is one of several, of differing molecular sizes, produced by

lues of the heat-stable enterotoxin ST-1.

C/Superfamily: heat-stable enterotoxin ST-1

C/Keywords: enterotoxin; heat-stable protein

F/1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>

F/5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 21.9%; Score 25; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCY 3  
|||  
Db 9 CCY 11

## RESULT 8

PC2248  
lambda.112 protein - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 17-Sep-1997  
C/Accession: PC2248  
R/Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isegawa, A.;  
Biochem. Biophys. Res. Commun. 198, 485-491, 1994  
A/Title: Krappe disease: isolation and characterization of a full-length cDNA for human  
A/Reference number: J02397; MUID:94128088; PMID:8297359  
A/Accession: PC2248  
A/Molecule type: mRNA  
A/Residues: 1-20 <SAK>  
A/Cross-references: DDBJ:D25284

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCY 3  
|||  
Db 5 CCY 7

## RESULT 9

A48389  
leiturtoxin III - Egyptian scorpion (fragment)  
C/Species: Leiurus quinquestriatus (Egyptian scorpion)  
C/Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
C/Accession: A48389  
R/Valdavia, H.H.; Martin, B.M.; Escobar, L.; Possani, L.D.  
Biochem. Int. 27, 953-962, 1992  
A/Title: Noxiustoxin and leiturtoxin II, two homologous peptide toxins with binding pro  
A/Reference number: A48389; MUID:93075256; PMID:1280139  
A/Accession: A48389  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <VAL>  
A/Experimental source: venom  
A/Note: sequence extracted from NCBI backbone (NCBIP:117118)

Query Match 21.1%; Score 24; DB 2; Length 14;  
Best Local Similarity 35.7%; Pred. No. 2.1e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 2 CYDGASVNDTCE 15  
|||  
Db 7 CYDSGQ-----CB 14

## RESULT 10

PD0002  
inulin fructotransferase (depolymerizing, difructofuranose-1,2',2,3'-dianhydride-forming  
C/Species: Bacillus sp.  
C/Date: 10-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 03-Jun-2002  
C/Accession: PD0002  
R/Kang, S.I.; Kim, W.P.; Chang, Y.J.; Kim, S.I.  
Biotech. Biochem. 62, 628-631, 1998  
A/Title: Purification and properties of inulin fructotransferase (PFA III-producing) fro  
A/Reference number: PD0002  
A/Accession: PD0002  
A/Molecule type: protein  
A/Residues: 1-16 <KAN>  
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 21.1%; Score 24; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 DGASVNDT 13  
|||  
Db 5 DGAPINQVNT 14

## RESULT 11

S28215  
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) GII - barley (fragment)  
N/Alternate names: (1-3)-beta-D-glucanase GII  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-Mar-1997 #sequence\_revision 17-Jul-1998 #text\_change 07-May-1999  
C/Accession: S28215  
R/Hrnova, M.; Fincher, G.B.  
Biochem. J. 289, 453-461, 1993  
A/Title: Purification and properties of three (1-3)-beta-D-glucanase isoenzymes from y  
A/Reference number: S28214; MUID:93143715; PMID:8424790  
A/Accession: S28215  
A/Molecule type: protein  
A/Residues: 1-12 <HRN>  
A/Experimental source: cultivar Clipper  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 20.2%; Score 23; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CYDGASVN 9  
|||  
Db 4 CYGIGINN 11

## RESULT 12

NTXNIM  
alpha-conotoxin MI - cone shell (Conus magus)  
C/Species: Conus magus (magus cone)  
C/Date: 18-Apr-1984 #sequence\_revision 18-Apr-1984 #text\_change 16-Jul-1999  
C/Accession: A01784  
R/McInosh, M.; Cruz, L.J.; Hunkapiller, M.W.; Gray, W.R.; Olivera, B.M.  
Arch. Biochem. Biophys. 218, 329-334, 1982  
A/Title: Isolation and structure of a peptide toxin from the marine snail Conus magus.  
A/Reference number: A90071; MUID:83073458; PMID:7149738  
A/Accession: A01784  
A/Molecule type: protein  
A/Residues: 1-14 <MCI>  
R/Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.  
J. Biol. Chem. 258, 12247-12251, 1983  
A/Title: Conotoxin MI. Disulfide bonding and conformational states.  
A/Reference number: A92396; MUID:84032400; PMID:6630287  
A/Contents: annotation: disulfide bonds  
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
C/Superfamily: alpha-conotoxin  
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F;3-8,4-14/disulfide bonds; #status experimental  
F;14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.2%; Score 23; DB 1; Length 14;  
Best Local Similarity 33.3%; Pred. No. 3e+03;  
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCYDGASVN 9  
|||  
Db 3 CCHPACGN 11

## RESULT 13

PH1317  
Ig heavy chain DJ region (clone C527-112) - human (fragment)  
C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C/Accession: PH1317  
 R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A/Title: Predominance of fetal type DHF joining in young children with B precursor lymphoma  
 A/Reference number: PH1302; MUID:93094761; PMID:1460419  
 A/Accession: PH1317  
 A/Molecule type: DNA  
 A/Residues: 1-16 <WAS>  
 C/Keywords: heterotrimer; immunoglobulin

Query Match 20.2%; Score 23; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYDAS 7  
 |||:  
 |||:  
 Db 5 CYGAST 10

RESULT 14  
 S60171  
 sex-lethal protein - fruit fly (Drosophila melanogaster) (fragment)  
 C/Species: Drosophila melanogaster  
 C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 17-Mar-1999  
 C/Accession: S60171  
 R/Hoshijima, K.; Kohyama, A.; Wataabe, I.; Inoue, K.; Sakamoto, H.; Shimura, Y.  
 Nucleic Acids Res. 23, 3441-3448, 1995  
 A/Title: Transcriptional regulation of the Sex-lethal gene by helix-loop-helix proteins.  
 A/Reference number: S60171; MUID:96032836; PMID:7567454  
 A/Accession: S60171  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-17 <HOS>  
 A/Cross-references: EMBL:D50435  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
 C/Genetics:  
 A/Gene: FlyBase:ScL  
 A/Cross-references: FlyBase:FBgn0003659

Query Match 20.2%; Score 23; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 3.6e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 TCORA 18  
 |||:  
 |||:  
 Db 12 TCORRS 17

RESULT 15  
 D49570  
 plasma membrane calcium pump - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 12-Dec-1997  
 C/Accession: D49570  
 R/Stautfer, T.P.; Hiltiker, H.; Garafoli, E.; Strehler, E.F.  
 J. Biol. Chem. 269, 25993-26003, 1993  
 A/Title: Quantitative analysis of alternative splicing options of human plasma membrane  
 A/Reference number: A49570; MUID:94064681; PMID:8245032  
 A/Accession: D49570  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-18 <STA>  
 A/Experimental source: cerebral cortex  
 A/Note: sequence inconsistent with nucleotide translation  
 A/Note: sequence extracted from NCBI backbone (NCBIN:139934, NCBIIP:139939)  
 C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C/Keywords: ATP

Query Match 20.2%; Score 23; DB 2; Length 18;  
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 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYDG 5  
 |||:  
 |||:  
 Db 5 CWDG 8

Search completed: December 9, 2003, 14:15:55  
 Job time : 21 secs